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(54) **PROTEIN SURFACE REMODELING**

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None

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(57) **ABSTRACT**

Aggregation is a major cause of the misbehavior of proteins. A system for modifying a protein to create a more stable variant is provided. The method involves identifying non-conserved hydrophobic amino acid residues on the surface of a protein, suitable for mutating to more hydrophilic residues (e.g., charged amino acids). Any number of residues on the surface may be changed to create a variant that is more soluble, resistant to aggregation, has a greater ability to re-fold, and/or is more stable under a variety of conditions. The invention also provides GFP, streptavidin, and GST variants with an increased theoretical net charge created by the inventive technology. Kits are also provided for carrying out such modifications on any protein of interest.

**26 Claims, 6 Drawing Sheets**

GFP (-30)	MGHHHHHGGASKGEEELPGVVPILVLEDGGVNGHEFVVRGEGGEDATEG
GFP (-25)	MGHHHHHGGASKGEEELPGVVPILVLEDGGVNGHEFVVRGEGGEDATEG
sGFP	MGHHHHHGGASKGEEELPGVVPILVLEDGGVNGHEFVVRGEGGEDATNG
GFP (+36)	MGHHHHHGGASKGEEELPGVVPILVLEDGGVNGHEFVVRGEGGEDATRG
GFP (+48)	MGHHHHHGGASKGEEELPGVVPILVLEDGGVNGHEFVVRGEGGEDATRG

GFP (-30)	KLTIKFICTTGELPVPWPVLVTTITYGVQCFSPYDHHMDQHDFFKSAMPE
GFP (-25)	KLTIKFICTTGELPVPWPVLVTTITYGVQCFSPYDHHMDQHDFFKSAMPE
sGFP	KLTIKFICTTGELPVPWPVLVTTITYGVQCFSPYDHHMDQHDFFKSAMPE
GFP (+36)	KLTIKFICTTGELPVPWPVLVTTITYGVQCFSPYDHHMDQHDFFKSAMPE
GFP (+48)	KLTIKFICTTGELPVPWPVLVTTITYGVQCFSPYDHHMDQHDFFKSAMPE

GFP (-30)	GYVQERTISFKDDGTYKTRAEVVFEGDTLVNRRILKGIIDFKEDGNILGKK
GFP (-25)	GYVQERTISFKDDGTYKTRAEVVFEGDTLVNRRILKGIIDFKEDGNILGKK
sGFP	GYVQERTISFKDDGTYKTRAEVVFEGDTLVNRRILKGIIDFKEDGNILGKK
GFP (+36)	GYVQERTISFKDDGTYKTRAEVVFEGDTLVNRRILKGIIDFKEDGNILGKK
GFP (+48)	GYVQERTISFKDDGTYKTRAEVVFEGDTLVNRRILKGIIDFKEDGNILGKK

GFP (-30)	LEYNPNSSHWITADKQNGIKAKETIRHNVEDGSGVQADHYQGNPTIGD
GFP (-25)	LEYNPNSSHWITADKQNGIKAKETIRHNVEDGSGVQADHYQGNPTIGD
sGFP	LEYNPNSSHWITADKQNGIKAKETIRHNVEDGSGVQADHYQGNPTIGR
GFP (+36)	LEYNPNSSHWITADKQNGIKAKETIRHNVEDGSGVQADHYQGNPTIGR
GFP (+48)	LEYNPNSSHWITADKQNGIKAKETIRHNVEDGSGVQADHYQGNPTIGR

GFP (-30)	GPVLLPDDHVLSTFESALSKDPNEGRDHMVILLEFVTAAGIDHGMDELYK
GFP (-25)	GPVLLPDDHVLSTFESALSKDPNEGRDHMVILLEFVTAAGIDHGMDELYK
sGFP	GPVLLPDDHVLSTFESALSKDPNEGRDHMVILLEFVTAAGIDHGMDELYK
GFP (+36)	GPVLLPDDHVLSTFESALSKDPNEGRDHMVILLEFVTAAGIDHGMDELYK
GFP (+48)	GPVLLPDDHVLSTFESALSKDPNEGRDHMVILLEFVTAAGIDHGMDELYK

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FIG. 1a-1
FIG. 1a-2

FIG. 1a

GFP (-30) MGH H H H H H G G A S K G E E L F D G V V P I L V E L D G D V N G H E F S V R G E G D A T E G  
GFP (-25) MGH H H H H H G G A S K G E E L F T G V V P I L V E L D G D V N G H E F S V R G E G D A T E G  
sfGFP MGH H H H H H G G A S K G E E L F T G V V P I L V E L D G D V N G H K F S V R G E G D A T N G  
GFP (+36) MGH H H H H H G G A S K G E R L F R G K V P I L V E L K G D V N G H K F S V R G K G D A T R G  
GFP (+48) MGH H H H H H G G R S K G R L F R G K V P I L V K L K G D V N G H K F S V R G K G D A T R G

GFP (-30) E L T L K F I C T T G E L P V P W P T L V T T I T Y G V Q C F S D Y P D H M D Q H D F F K S A M P E  
GFP (-25) E L T L K F I C T T G E L P V P W P T L V T T I T Y G V Q C F S R Y P D H M K Q H D F F K S A M P E  
sfGFP K I T L K F I C T T G K L P V P W P T L V T T I T Y G V Q C F S R Y P D H M K Q H D F F K S A M P E  
GFP (+36) K I T L K F I C T T G K L P V P W P T L V T T I T Y G V Q C F S R Y P K H M K R H D F F K S A M P K  
GFP (+48) K I T L K F I C T T G K L P V P W P T L V T T I T Y G V Q C F S R Y P K H M K R H D F F K S A M P K

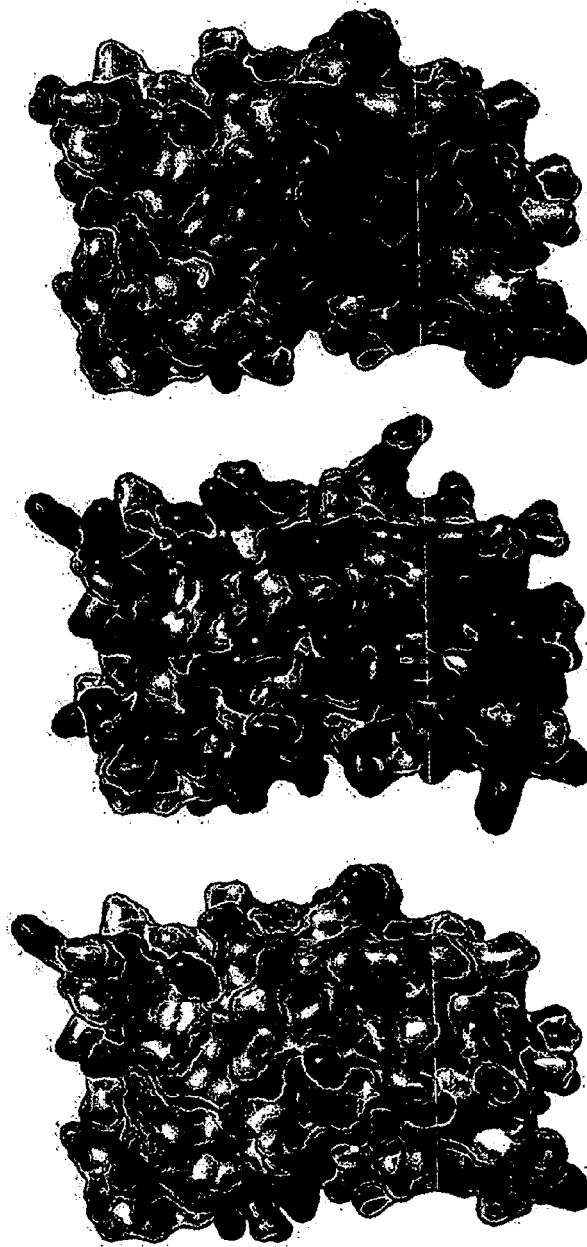
GFP (-30) G Y V Q E R T I S E K D D G T Y K T R A E V K F E G D T L V N R I E L K G I D F K E D G N I L G H K  
GFP (-25) G Y V Q E R T I S E K D D G T Y K T R A E V K F E G D T L V N R I E L K G I D F K E D G N I L G H K  
sfGFP G Y V Q E R T I S E K D D G T Y K T R A E V K F E G D T L V N R I E L K G I D F K E D G N I L G H K  
GFP (+36) G Y V Q E R T I S E K K D G K Y K T R A E V K F E G R T L V N R I K L K C R D F K E K G N I L G H K  
GFP (+48) G Y V Q E R T I S E K K D G K Y K T R A E V K F K G R T L V N R I K L K C R D F K E K G N I L G H K

GFP (-30) L E Y N F N S H D V Y I T A D K Q E N G I K A E F E I R H N V E D G S V Q L A D H Y Q Q N T P I G D  
GFP (-25) L E Y N F N S H D V Y I T A D K Q E N G I K A E F E I R H N V E D G S V Q L A D H Y Q Q N T P I G D  
sfGFP L E Y N F N S H N V Y I T A D K Q K N G I K A N F K I R H N V E D G S V Q L A D H Y Q Q N T P I G D  
GFP (+36) L R Y N F N S H K V Y I T A D K R K N G I K A K F K I R H N V K D G S V Q L A D H Y Q Q N T P I G R  
GFP (+48) L R Y N F N S H K V Y I T A D K R K N G I K A K F K I R H N V K D G S V Q L A K H Y Q Q N T P I G R

FIG. 1a-1

GFP (-30)	GPVLLP	D	D	H	Y	L	S	T	E	S	A	L	S	K	D	P	N	E	D	R	D	H	M	V	L	L	E	F	V	T	A	A	G	I	D	H	G	M	D	E	L	Y	K					
GFP (-25)	GPVLLP	D	D	H	Y	L	S	T	E	S	A	L	S	K	D	P	N	E	D	R	D	H	M	V	L	L	L	E	F	V	T	A	A	G	I	D	H	G	M	D	E	L	Y	K				
sfGFP	GPVLLP	D	N	H	Y	L	S	T	Q	S	A	L	S	K	D	P	N	E	K	R	D	H	M	V	L	L	L	L	E	F	V	T	A	A	G	I	T	H	G	M	D	E	L	Y	K			
GFP (+36)	GPVLLP	R	N	H	Y	L	S	T	R	S	K	L	S	K	D	P	K	E	K	R	D	H	M	V	L	L	L	L	L	E	F	V	T	A	A	G	I	R	H	G	R	D	E	F	Y	K		
GFP (+48)	GPVLLP	R	K	H	Y	L	S	T	R	S	K	L	S	K	D	P	K	E	K	R	D	H	M	V	L	L	L	L	L	L	L	E	F	V	T	A	A	G	I	K	H	G	R	K	E	R	Y	K

FIG. 1a-2



sfGFP

GFP(+36)

GFP(-30)

FIG. 1b

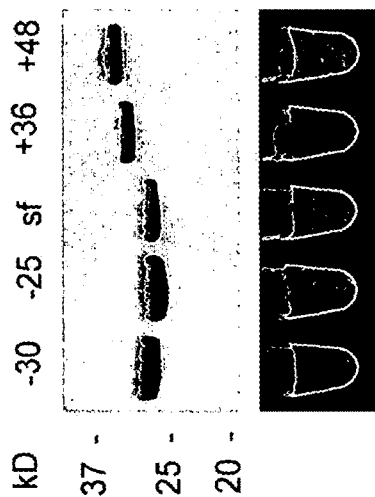


FIG. 2a

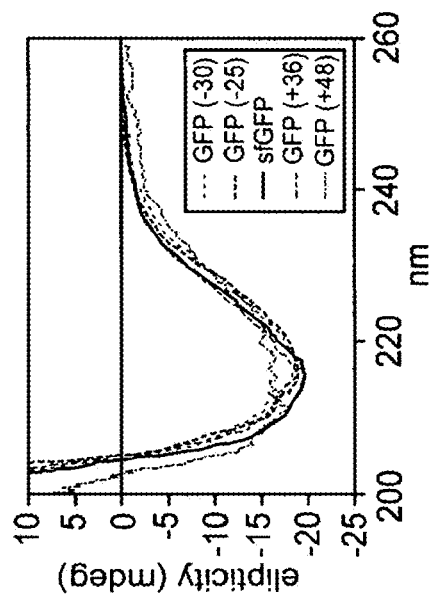


FIG. 2b

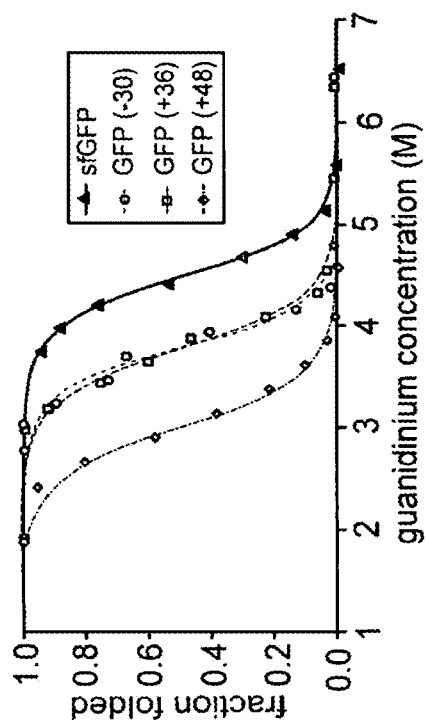


FIG. 2c

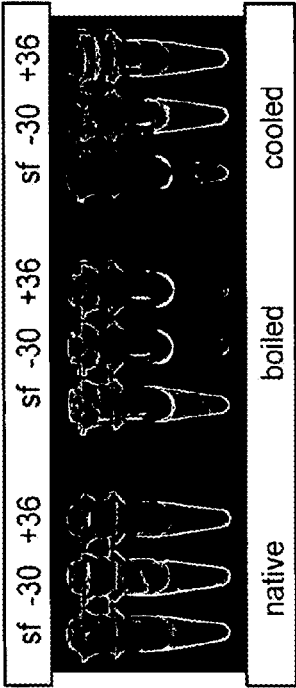


FIG. 3a

GFP (+36)	+	+	+	+	+	+	+	-	-	-
sfGFP	-	-	-	-	-	-	-	+	+	+
GFP (-30)	-	+	-	-	-	-	-	+	+	-
DNA	-	-	+	-	-	-	-	-	-	-
tRNA	-	-	-	+	+	+	+	-	-	+
NaCl	-	-	-	-	-	-	-	-	-	-
	1	2	3	4	5	6	7	8		

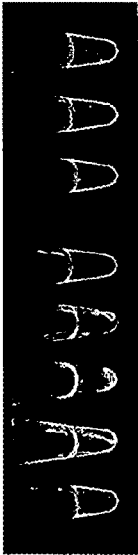


FIG. 3c

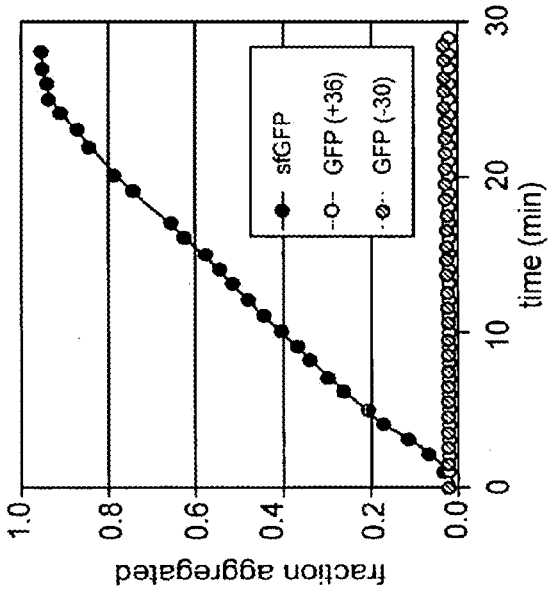


FIG. 3b

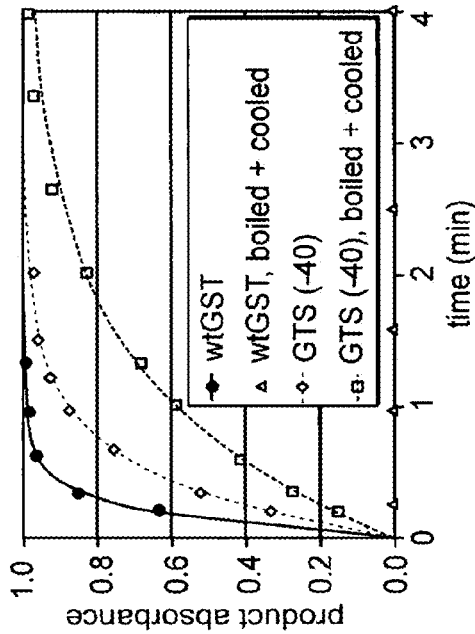


FIG. 3d

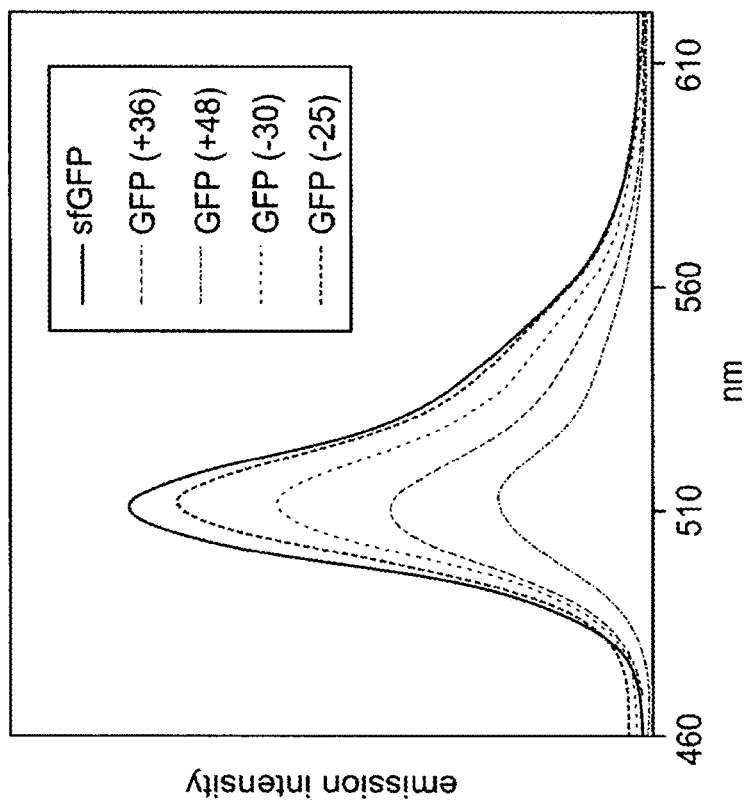


FIG. 4a

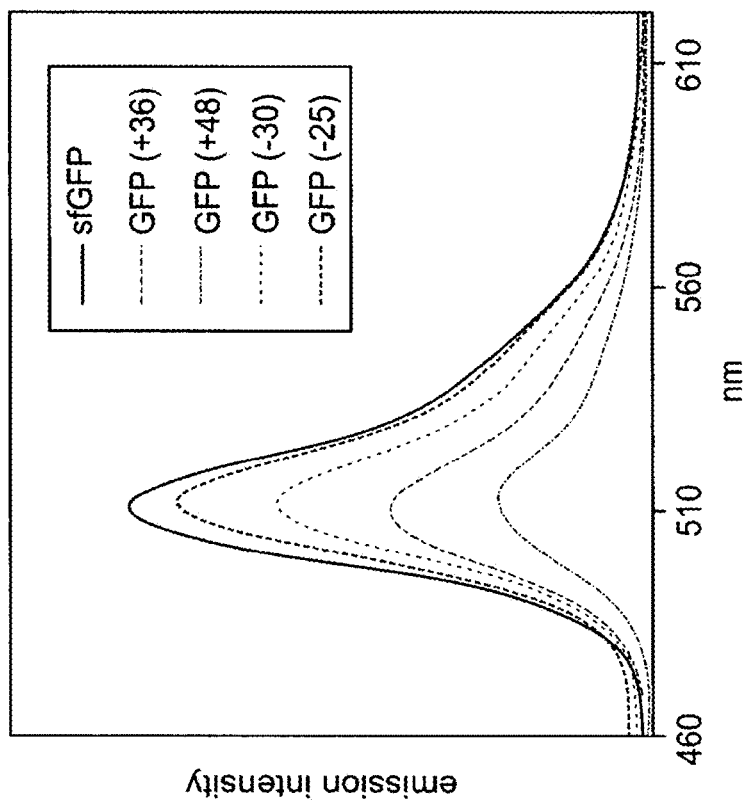


FIG. 4b

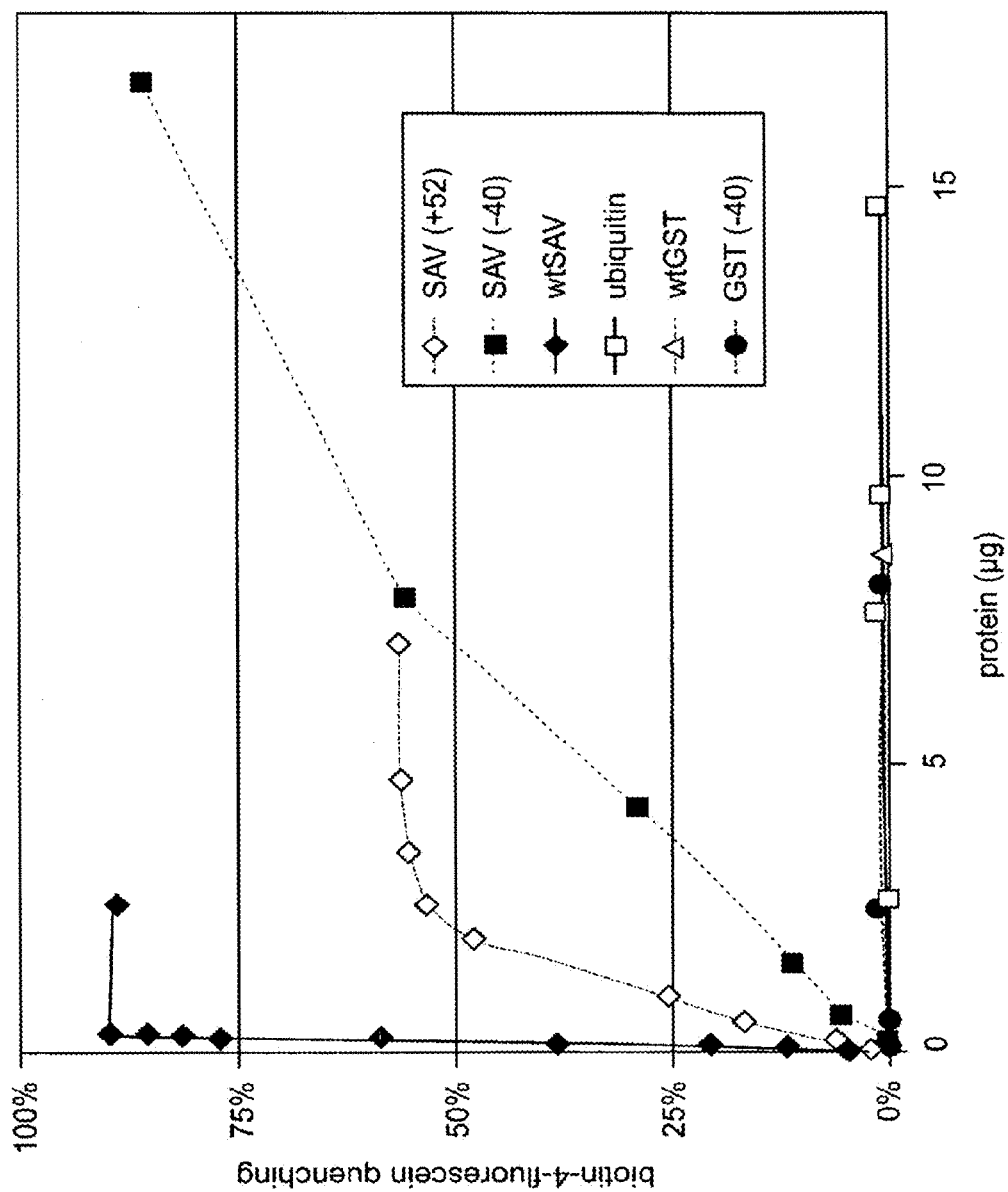


FIG. 5

**PROTEIN SURFACE REMODELING****RELATED APPLICATIONS**

The present application claims priority under 35 U.S.C. §120 to and is a continuation of U.S. patent application, U.S. Ser. No. 12/303,047, filed Mar. 9, 2010, which is a national stage filing under 35 U.S.C. §371 of international PCT application, PCT/US2007/070254, filed Jun. 1, 2007, which claims priority under 35 U.S.C. §119(e) to U.S. provisional patent applications, U.S. Ser. No. 60/810,364, filed Jun. 2, 2006, and U.S. Ser. No. 60/836,607, filed Aug. 9, 2006; each of which is incorporated herein by reference.

**GOVERNMENT SUPPORT**

The work described herein was supported, in part, by grants from the National Institutes of Health (GM065400). The United States government may have certain rights in the invention.

**BACKGROUND OF THE INVENTION**

Proteins are the workhorses of the cell. Proteins catalyze chemical reactions, transduce signals in biological systems, provide structural elements in cells and the extracellular matrix, act as messengers, etc. One of the major causes of misbehavior of proteins is aggregation. This is not only a problem in the laboratory but also a problem in many diseases such as Alzheimer's disease. Aggregation is a particularly vexing problem when it comes to computationally designed proteins. For example, TOP7 is a computationally designed protein with a novel fold. A longer version of TOP7, TOP7 extended, is very prone to aggregation. TOP7ex is expressed predominantly as insoluble aggregates.

As more proteins are either designed or modified to be used as tools to study biological systems or as more proteins—wild type or modified—are used as therapeutic agents, there needs to be a system for routinely modifying these proteins to be more stable and/or to prevent aggregation.

**SUMMARY OF THE INVENTION**

The present invention provides a system for modifying proteins to make them more stable. The invention stems from the recognition that modifying the hydrophobic areas on the surface of a protein can improve the extrathermodynamic properties of the protein. The inventive system is particularly useful in improving the solubility of a protein of interest, improving the protein's resistance to aggregation, and/or improving the protein's ability to renature. All of these properties are particularly useful in protein production, protein purification, and the use of proteins as therapeutic agents and research tools.

In one aspect, the invention provides a method of altering the primary sequence of a protein in order to increase the protein's resistance to aggregation, solubility, ability to refold, and/or general stability under a wide range of conditions. The activity of the modified protein is preferably approximately or substantially the same as the protein without modification. In certain embodiments, the modified protein retains at least 50%, 75%, 90%, or 95% of the wild type protein's activity. In one embodiment, the method includes the steps of (a) identifying the surface residues of a protein of interest; (b) identifying the particular surface residues that are not highly conserved among other proteins

related to the protein of interest (i.e., determining which amino acids are not essential for the activity or function of the protein); (c) determining the hydrophobicity of the identified non-conserved surface residues; and (e) replacing at least one or more of the identified hydrophobic, non-conserved residues with an amino acid that is more polar or is charged at physiological pH. Each of the above steps may be carried out using any technique, computer software, algorithm, paradigm, etc. known in the art. After the modified protein is created, it may be tested for its activity and/or the desired property being sought. In certain embodiments, the modified protein is more stable. In certain embodiments, the modified protein is less susceptible to aggregation. The inventive method typically increases the net charge (positive or negative) on the protein at physiological pH.

In another aspect, the invention provides a method of altering the primary sequence of a protein in order to increase the protein's resistance to aggregation, solubility, ability to refold, and/or general stability under a wide range of conditions by "supercharging" the protein. That is, the overall net charge on the modified protein is increased (either positive charge or negative charge) compared to the wild type protein. Preferably, the activity of the modified protein is approximately or substantially the same as the protein without modification. In certain embodiments, the method includes the steps of (a) identifying the surface residues of a protein of interest; (b) identifying the particular surface residues that are not highly conserved among other proteins related to the protein of interest (i.e., determining which amino acids are not essential for the activity or function of the protein); (c) determining the hydrophilicity of the identified non-conserved surface residues; and (e) replacing at least one or more of the identified charged or polar, solvent-exposed, non-conserved residues with a charged amino acid that is charged at physiological pH. In certain embodiments, to make a negatively charged "supercharged" protein, the residues identified for modification are mutated either to aspartate (Asp) or glutamate (Glu) residues. In certain other embodiments, to make a positively charged "supercharged" protein, the residues identified for modification are mutated either to lysine (Lys) or arginine (Arg) residues. Each of the above steps may be carried out using any technique, computer software, algorithm, paradigm, etc. known in the art. After the modified protein is created, it may be tested for its activity and/or the desired property being sought. In certain embodiments, the modified protein ("supercharged protein") is more stable. In certain embodiments, the modified protein is less susceptible to aggregation. The inventive method typically increases the net charge (positive or negative) on the protein at physiological pH.

The theoretical net charge on over 80% of the proteins catalogued in the Protein Data Bank (PDB) fall within  $\pm 10$ . The modified protein created by the present invention typically have a net charge less than  $-10$  or greater than  $+10$ . In certain embodiments, the modified protein has a net charge less than  $-20$  or greater than  $+20$ . In certain embodiments, the modified protein has a net charge less than  $-30$  or greater than  $+30$ . In certain embodiments, the modified protein has a net charge less than  $-40$  or greater than  $+40$ . In certain embodiments, the modified protein has a net charge less than  $-50$  or greater than  $+50$ . The modified proteins are able to fold correctly and retain their biological activity.

Any protein may be modified using the inventive system, and protein variants created by the inventive system are considered to be part of the present invention, as well as polynucleotides or vectors encoding the variant protein and

cells expressing the variant protein. The inventive system has been used to create several new variants of green fluorescent protein (GFP). These variants retain their fluorescence; however, they are more stable than current versions of GFP under a wide range of environments. The inventive GFPs are immune to aggregation even over long periods of time and in environments that induce aggregation and are capable of refolding into a fluorescent protein even after being denatured by boiling. The inventive system has also been used to create new variants of streptavidin and glutathione-S-transferase (GST). These variants retain their biological activity and remain soluble when heated. The invention also includes polynucleotide sequences encoding the inventive GFP, streptavidin, and GST protein sequences, vectors including any of these nucleotide sequences, and cells that include such a polynucleotide sequence or vector, or express the inventive variants. In certain embodiments, the invention includes bacteria or other cells that overexpress an inventive variant. The inventive variants may be used in a variety of biological assays known in the art. For example, supercharged GFPs may be used in any assay that currently uses GFP as a reporter protein.

In another aspect, the invention provides other proteins that have been modified by the inventive system. These modified proteins preferably retain a significant portion of their original activity. In certain embodiments, the modified protein retains at least 99%, 98%, 95%, or 90% of the activity of the unmodified version. The modified protein may be more soluble, resistant to aggregation, have a increased ability to refold, and/or have greater stability under a variety of conditions. The proteins modified by the inventive system include hydrophobic proteins, recombinant proteins, membrane proteins, structural proteins, enzymes, extracellular proteins, therapeutic proteins (e.g., insulin, cytokines, immunoglobulins, fragments of immunoglobulins, etc.), receptors, cell signaling proteins, cytoplasmic proteins, nuclear proteins, transcription factors, etc. In certain specific embodiments, the proteins are therapeutic proteins for use in human or veterinary medicine. In certain embodiments, the proteins are unnatural proteins, for example, computationally designed proteins. In other embodiments, the proteins are hybrid proteins, fusion proteins, altered proteins, mutated proteins, genetically engineered proteins, or any other protein that has been altered by the hands of man.

Kits are also provided for the practice of the invention. The kits may include the reagents needed to modify a protein of interest to make it more resistant to aggregation, increase its ability to renature, or increase its stability overall. Such kits may include all or some of the following: polynucleotides, computer software, nucleotides, primers, vectors, cell lines, instructions, plates, media, buffers, enzymes, Eppendorf tubes, site-directed mutagenesis kits, etc. Preferably, the kit is conveniently packaged for use in a laboratory setting. The researcher typically provides the DNA coding sequence of the protein to be modified using the inventive technique.

#### DEFINITIONS

“Amino acid”: The term “amino acid” refers to the basic structural subunits of proteins. An alpha-amino acid consists of an amino group, a carboxyl group, a hydrogen atom, and a side chain (i.e., R group) all bonded to a central carbon atom. This central carbon atom is referred to as the alpha carbon because it is adjacent to the carboxyl group. There are twenty natural amino acids including glycine, alanine, valine, leucine, isoleucine, phenylalanine, tyrosine, tryptophan, cysteine, methionine, serine, threonine, lysine, arginine, histidine, aspartate, glutamate, asparagine, glutamine, and proline. Hydrophobic amino acids include alanine, valine, leucine, isoleucine, and phenylalanine. Aromatic amino acids include phenylalanine, tyrosine, tryptophan, and histidine. Polar amino acids include tyrosine, cysteine, serine, threonine, lysine, arginine, histidine, aspartate, glutamate, asparagine, and glutamine. Sulfur-containing amino acids include cysteine and methionine. Basic amino acids include lysine, arginine, and histidine. Acidic amino acids include aspartate and glutamate. Unnatural amino acids have also been inserted into proteins. In certain embodiments, the twenty natural amino acids are referred to when the term “amino acid” is used.

“Antibody”: The term “antibody” refers to an immunoglobulin, whether natural or wholly or partially synthetically produced. All derivatives thereof which maintain specific binding ability are also included in the term. The term also covers any protein having a binding domain which is homologous or largely homologous to an immunoglobulin binding domain. These proteins may be derived from natural sources, or partly or wholly synthetically produced. An antibody may be monoclonal or polyclonal. The antibody may be a member of any immunoglobulin class, including any of the human classes: IgG, IgM, IgA, IgD, and IgE.

“Conserved”: The term “conserved” refers nucleotides or amino acid residues of a polynucleotide sequence or amino acid sequence, respectively, that are those that occur unaltered in the same position of two or more related sequences being compared. Nucleotides or amino acids that are relatively conserved are those that are conserved amongst more related sequences than nucleotides or amino acids appearing elsewhere in the sequences.

“Homologous”: The term “homologous”, as used herein is an art-understood term that refers to nucleic acids or proteins that are highly related at the level of nucleotide or amino acid sequence. Nucleic acids or proteins that are homologous to each other are termed homologues. Homologous may refer to the degree of sequence similarity between two sequences (i.e., nucleotide sequence or amino acid). The homology percentage figures referred to herein reflect the maximal homology possible between two sequences, i.e., the percent homology when the two sequences are so aligned as to have the greatest number of matched (homologous) positions. Homology can be readily calculated by known methods such as those described in: Computational Molecular Biology, Lesk, A. M., ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, Smith, D. W., ed., Academic Press, New York, 1993; Sequence Analysis in Molecular Biology, von Heinje, G., Academic Press, 1987; Computer Analysis of Sequence Data, Part I, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; and Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; each of which is incorporated herein by reference. Methods commonly employed to determine homology between sequences include, but are not limited to those disclosed in Carillo, H., and Lipman, D., SIAM J Applied Math., 48:1073 (1988); incorporated herein by reference. Techniques for determining homology are codified in publicly available computer programs. Exemplary computer software to determine homology between two sequences include, but are not limited to, GCG program package, Devereux, J., et al., Nucleic Acids Research, 12(1), 387 (1984)), BLASTP, BLASTN, and FASTA Atschul, S. F. et al., J Molec. Biol., 215, 403 (1990)).



The term “homologous” necessarily refers to a comparison between at least two sequences (nucleotide sequences or amino acid sequences). In accordance with the invention, two nucleotide sequences are considered to be homologous if the polypeptides they encode are at least about 50-60% identical, preferably about 70% identical, for at least one stretch of at least 20 amino acids. Preferably, homologous nucleotide sequences are also characterized by the ability to encode a stretch of at least 4-5 uniquely specified amino acids. Both the identity and the approximate spacing of these amino acids relative to one another must be considered for nucleotide sequences to be considered homologous. For nucleotide sequences less than 60 nucleotides in length, homology is determined by the ability to encode a stretch of at least 4-5 uniquely specified amino acids.

“Peptide” or “protein”: According to the present invention, a “peptide” or “protein” comprises a string of at least three amino acids linked together by peptide bonds. The terms “protein” and “peptide” may be used interchangeably. Inventive peptides preferably contain only natural amino acids, although non-natural amino acids (i.e., compounds that do not occur in nature but that can be incorporated into a polypeptide chain) and/or amino acid analogs as are known in the art may alternatively be employed. Also, one or more of the amino acids in an inventive peptide may be modified, for example, by the addition of a chemical entity such as a carbohydrate group, a phosphate group, a farnesyl group, an isofarnesyl group, a fatty acid group, a linker for conjugation, functionalization, or other modification (e.g., alpha amidation), etc. In a preferred embodiment, the modifications of the peptide lead to a more stable peptide (e.g., greater half-life in vivo). These modifications may include cyclization of the peptide, the incorporation of D-amino acids, etc. None of the modifications should substantially interfere with the desired biological activity of the peptide. In certain embodiments, the modifications of the peptide lead to a more biologically active peptide.

“Polynucleotide” or “oligonucleotide”: Polynucleotide or oligonucleotide refers to a polymer of nucleotides. Typically, a polynucleotide comprises at least three nucleotides. The polymer may include natural nucleosides (i.e., adenosine, thymidine, guanosine, cytidine, uridine, deoxyadenosine, deoxythymidine, deoxyguanosine, and deoxycytidine), nucleoside analogs (e.g., 2-aminoadenosine, 2-thiothymidine, inosine, pyrrolo-pyrimidine, 3-methyl adenosine, C5-propynylcytidine, C5-propynyluridine, C5-bromouridine, C5-fluorouridine, C5-iodouridine, C5-methylcytidine, 7-deazaadenosine, 7-deazaguanosine, 8-oxoadenosine, 8-oxoguanosine, O(6)-methylguanine, and 2-thiocytidine), chemically modified bases, biologically modified bases (e.g., methylated bases), intercalated bases, modified sugars (e.g., 2'-fluororibose, ribose, 2'-deoxyribose, arabinose, and hexose), and/or modified phosphate groups (e.g., phosphorothioates and 5'-N-phosphoramidite linkages).

“Small molecule”: The term “small molecule,” as used herein, refers to a non-peptidic, non-oligomeric organic compound either prepared in the laboratory or found in nature. Small molecules, as used herein, can refer to compounds that are “natural product-like,” however, the term “small molecule” is not limited to “natural product-like” compounds. Rather, a small molecule is typically characterized in that it contains several carbon-carbon bonds, and has a molecular weight of less than 1500, although this characterization is not intended to be limiting for the purposes of the present invention. In certain other preferred embodiments, natural-product-like small molecules are utilized.

“Stable”: The term “stable” as used herein to refer to a protein refers to any aspect of protein stability. The stable modified protein as compared to the original wild type protein possesses any one or more of the following characteristics: more soluble, more resistant to aggregation, more resistant to denaturation, more resistant to unfolding, more resistant to improper or undesired folding, greater ability to renature, increased thermal stability, increased stability in a variety of environments (e.g., pH, salt concentration, presence of detergents, presence of denaturing agents, etc.), and increased stability in non-aqueous environments. In certain embodiments, the stable modified protein exhibits at least two of the above characteristics. In certain embodiments, the stable modified protein exhibits at least three of the above characteristics. Such characteristics may allow the active protein to be produced at higher levels. For example, the modified protein can be overexpressed at a higher level without aggregation than the unmodified version of the protein. Such characteristics may also allow the protein to be used as a therapeutic agent or a research tool.

#### BRIEF DESCRIPTION OF THE DRAWING

FIG. 1. Supercharged green fluorescent proteins (GFPs).

(a) Protein sequences of GFP variants, with fluorophore-forming residues highlighted green, negatively charged residues highlighted red, and positively charged residues highlighted blue. GFP-30 (SEQ ID NO: 24); GFP-25 (SEQ ID NO: 25); sfGFP (SEQ ID NO: 26); GFP+36 (SEQ ID NO: 5); GFP+48 (SEQ ID NO: 27). (b) Electrostatic surface potentials of sfGFP (left), GFP(+36) (middle), and GFP(−30) (right), colored from −25 kT/e (red) to +25 kT/e (blue).

FIG. 2. Intramolecular properties of GFP variants. (a) Staining and UV fluorescence of purified GFP variants. Each lane and tube contains 0.2 μg of protein. (b) Circular dichroism spectra of GFP variants. (c) Thermodynamic stability of GFP variants, measured by guanidinium-induced unfolding.

FIG. 3. Intermolecular properties of supercharged proteins. (a) UV-illuminated samples of purified GFP variants (“native”), those samples heated 1 min at 100° C. (“boiled”), and those samples subsequently cooled for 2 h at 25° C. (“cooled”). (b) Aggregation of GFP variants was induced with 40% TFE at 25° C. and monitored by right-angle light scattering. (c) Supercharged GFPs adhere reversibly to oppositely charged macromolecules. Sample 1: 6 μg of GFP(+36) in 30 μl of 25 mM Tris pH 7.0 and 100 mM NaCl. Sample 2: 6 μg of GFP(−30) added to sample 1. Sample 3: 30 μg of salmon sperm DNA added to sample 1. Sample 4: 20 μg of *E. coli* tRNA added to sample 1. Sample 5: Addition of NaCl to 1 M to sample 4. Samples 6-8: identical to samples 1, 2, and 4, respectively, except using sfGFP instead of GFP(+36). All samples were spun briefly in a microcentrifuge and visualized under UV light. (d) Enzymatic assays of GST variants. Reactions contained 0.5 mg/mL of GST variant, 20 mM chlorodinitrobenzene, 20 mM glutathione, and 100 mM potassium phosphate pH 6.5. Product formation was monitored at 340 nm, resulting in observed reaction rates ( $k_{obs}$ ) of 6 min<sup>−1</sup> for wild-type GST, 2.2 min<sup>−1</sup> for GST(−40), and 0.9 min<sup>−1</sup> for GST(−40) after being boiled and cooled.

FIG. 4. (a) Excitation and (b) emission spectra of GFP variants. Each sample contained an equal amount of protein as quantitated by chromophore absorbance at 490 nm.

FIG. 5. Biotin-binding activity of streptavidin variants, measured as described previously (Kada et al., Rapid estimation of avidin and streptavidin by fluorescence quenching

or fluorescence polarization. *Biochim. Biophys. Acta* 1427, 44-48 (1999); incorporated herein by reference) by monitoring binding-dependent of biotin-4-fluorescein (Invitrogen). Protein samples were titrated into 0.3  $\mu$ M biotin-4-fluorescein (B4F), 100 mM NaCl, 1 mM EDTA, 0.1 mg/mL bovine serum albumin (BSA), 50 mM potassium phosphate pH 7.5. Quenching of fluorescence at 526 nm was measured on a Perkin-Elmer LS50B luminescence spectrometer with excitation at 470 nm. Measurements were normalized to control titrations that contained a 600-fold excess of non-fluorescent biotin. The three proteins in the bottom of the legend are included as negative controls.

#### DETAILED DESCRIPTION OF CERTAIN PREFERRED EMBODIMENTS OF THE INVENTION

The invention provides a system for modifying proteins to be more stable. The system is thought to work by changing non-conserved amino acids on the surface of a protein to more polar or charged amino acid residues. The amino acids residues to be modified may be hydrophobic, hydrophilic, charged, or a combination thereof. Any protein may be modified using the inventive system to produce a more stable variant. These modifications of surface residues have been found to improve the extrathermodynamic properties of proteins. As proteins are increasingly used as therapeutic agents and as they continue to be used as research tools, a system for altering a protein to make it more stable is important and useful. Proteins modified by the inventive method typically are resistant to aggregation, have an increased ability to refold, resist improper folding, have improved solubility, and are generally more stable under a wide range of conditions including denaturing conditions such as heat or the presence of a detergent.

Any protein may be modified to create a more stable variant using the inventive system. Natural as well as unnatural proteins (e.g., engineered proteins) may be modified. Example of proteins that may be modified include receptors, membrane bound proteins, transmembrane proteins, enzymes, transcription factors, extracellular proteins, therapeutic proteins, cytokines, messenger proteins, DNA-binding proteins, RNA-binding proteins, proteins involved in signal transduction, structural proteins, cytoplasmic proteins, nuclear proteins, hydrophobic proteins, hydrophilic proteins, etc. The protein to be modified may be derived from any species of plant, animal, or microorganism. In certain embodiments, the protein is a mammalian protein. In certain embodiments, the protein is a human protein. In certain embodiments, the proteins is derived from an organism typically used in research. For example, the protein to be modified may be from a primate (e.g., ape, monkey), rodent (e.g., rabbit, hamster, gerbil), pig, dog, cat, fish (e.g., zebrafish), nematode (e.g., *C. elegans*), yeast (e.g., *Saccharomyces cerevisiae*), or bacteria (e.g., *E. coli*).

The inventive system is particularly useful in modifying proteins that are susceptible to aggregation or have stability issues. The system may also be used to modify proteins that are being overexpressed. For example, therapeutic proteins that are being produced recombinantly may benefit from being modified by the inventive system. Such modified therapeutic proteins are not only easier to produce and purify but also may be more stable with respect to storage and use of the protein.

The inventive system involves identifying non-conserved surface residues of a protein of interest and replacing some of those residues with a residue that is hydrophilic, polar, or

charged at physiological pH. The inventive system includes not only methods for modifying a protein but also reagents and kits that are useful in modifying a protein to make it more stable.

The surface residues of the protein to be modified are identified using any method(s) known in the art. In certain embodiments, the surface residues are identified by computer modeling of the protein. In certain embodiments, the three-dimensional structure of the protein is known and/or determined, and the surface residues are identified by visualizing the structure of the protein. In other embodiments, the surface residues are predicted using computer software. In certain particular embodiments, Average Neighbor Atoms per Sidechain Atom (AvNAPSA) is used to predict surface exposure. AvNAPSA is an automated measure of surface exposure which has been implemented as a computer program. See Appendix A. A low AvNAPSA value indicates a surface exposed residue, whereas a high value indicates a residue in the interior of the protein. In certain embodiments, the software is used to predict the secondary structure and/or tertiary structure of a protein and the surface residues are identified based on this prediction. In other embodiments, the prediction of surface residues is based on hydrophobicity and hydrophilicity of the residues and their clustering in the primary sequence of the protein. Besides in silico methods, the surface residues of the protein may also be identified using various biochemical techniques, for example, protease cleavage, surface modification, etc.

Of the surface residues, it is then determined which are conserved or important to the functioning of the protein. The identification of conserved residues can be determined using any method known in the art. In certain embodiments, the conserved residues are identified by aligning the primary sequence of the protein of interest with related proteins. These related proteins may be from the same family of proteins. For example, if the protein is an immunoglobulin, other immunoglobulin sequences may be used. The related proteins may also be the same protein from a different species. For example, the conserved residues may be identified by aligning the sequences of the same protein from different species. To give but another example, proteins of similar function or biological activity may be aligned. Preferably, 2, 3, 4, 5, 6, 7, 8, 9, or 10 different sequences are used to determine the conserved amino acids in the protein. In certain embodiments, the residue is considered conserved if over 50%, 60%, 70%, 75%, 80%, or 90% of the sequences have the same amino acid in a particular position. In other embodiments, the residue is considered conserved if over 50%, 60%, 70%, 75%, 80%, or 90% of the sequences have the same or a similar (e.g., valine, leucine, and isoleucine; glycine and alanine; glutamine and asparagine; or aspartate and glutamate) amino acid in a particular position. Many software packages are available for aligning and comparing protein sequences as described herein. As would be appreciated by one of skill in the art, either the conserved residues may be determined first or the surface residues may be determined first. The order does not matter. In certain embodiments, a computer software package may determine surface residues and conserved residues simultaneously. Important residues in the protein may also be identified by mutagenesis of the protein. For example, alanine scanning of the protein can be used to determine the important amino acid residues in the protein. In other embodiments, site-directed mutagenesis may be used.

Once non-conserved surface residues of the protein have been identified, each of the residues is identified as hydrophobic or hydrophilic. In certain embodiments, the residues

is assigned a hydrophobicity score. For example, each non-conserved surface residue may be assigned an octanol/water log P value. Other hydrophobicity parameters may also be used. Such scales for amino acids have been discussed in: Janin, "Surface and Inside Volumes in Globular Proteins," *Nature* 277:491-92, 1979; Wolfenden et al., "Affinities of Amino Acid Side Chains for Solvent Water," *Biochemistry* 20:849-855, 1981; Kyte et al., "A Simple Method for Displaying the Hydrophobic Character of a Protein," *J. Mol. Biol.* 157:105-132, 1982; Rose et al., "Hydrophobicity of Amino Acid Residues in Globular Proteins," *Science* 229:834-838, 1985; Cornette et al., "Hydrophobicity Scales and Computational Techniques for Detecting Amphipathic Structures in Proteins," *J. Mol. Biol.* 195:659-685, 1987; Charton and Charton, "The Structure Dependence of Amino Acid Hydrophobicity Parameters," *J. Theor. Biol.* 99:629-644, 1982; each of which is incorporated by reference. Any of these hydrophobicity parameters may be used in the inventive method to determine which non-conserved residues to modify. In certain embodiments, hydrophilic or charged residues are identified for modification.

At least one identified non-conserved or non-vital surface residue is then chosen for modification. In certain embodiments, hydrophobic residue(s) are chosen for modification. In other embodiments, hydrophilic and/or charged residue(s) are chosen for modification. In certain embodiments, more than one residue is chosen for modification. In certain embodiments, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 of the identified residues are chosen for modification. In certain embodiments, over 10, over 15, or over 20 residues are chosen for modification. As would be appreciated by one of skill in the art, the larger the protein the more residues that will need to be modified. Also, the more hydrophobic or susceptible to aggregation or precipitation the protein is, the more residues will need to be modified. In certain embodiments, multiple variants of the protein, each with different modifications, are produced and tested to determine the best variant in terms of biological activity and stability.

In certain embodiments, the residues chosen for modification are mutated into more hydrophilic residues (including charged residues). Typically, the residues are mutated into more hydrophilic natural amino acids. In certain embodiments, the residues are mutated into amino acids that are charged at physiological pH. For example, the residue may be changed to an arginine, aspartate, glutamate, histidine, or lysine. In certain embodiments, all the residues to be modified are changed into the same different residue. For example, all the chosen residues are changed to a glutamate residue. In other embodiments, the chosen residues are changed into different residues; however, all the final residues may be either positively charged or negatively charged at physiological pH. In certain embodiments, to create a negatively charged protein, all the residues to be mutated are converted to glutamate and/or aspartate residues. In certain embodiments, to create a positively charged protein, all the residues to be mutated are converted to lysine residues. For example, all the chosen residues for modification are asparagine, glutamine, lysine, and/or arginine, and these residues are mutated into aspartate or glutamate residues. To give but another example, all the chosen residues for modification are aspartate, glutamate, asparagine, and/or glutamine, and these residues are mutated into lysine. This approach allows for modifying the net charge on the protein to the greatest extent.

In other embodiments, the protein may be modified to keep the net charge on the modified protein the same as on

the unmodified protein. In still other embodiments, the protein may be modified to decrease the overall net charge on the protein while increasing the total number of charged residues on the surface. In certain embodiments, the theoretical net charge is increased by at least +1, +2, +3, +4, +5, +10, +15, +20, +25, +30, or +35. In certain embodiments, the theoretical net charge is decreased by at least -1, -2, -3, -4, -5, -10, -15, -20, -25, -30, or -35. In certain embodiments, the chosen amino acids are changed into non-ionic, polar residues (e.g., cysteine, serine, threonine, tyrosine, glutamine, asparagine).

These modification or mutations in the protein may be accomplished using any technique known in the art. Recombinant DNA techniques for introducing such changes in a protein sequence are well known in the art. In certain embodiments, the modifications are made by site-directed mutagenesis of the polynucleotide encoding the protein. Other techniques for introducing mutations are discussed in *Molecular Cloning: A Laboratory Manual*, 2nd Ed., ed. by Sambrook, Fritsch, and Maniatis (Cold Spring Harbor Laboratory Press: 1989); the treatise, *Methods in Enzymology* (Academic Press, Inc., N.Y.); Ausubel et al. *Current Protocols in Molecular Biology* (John Wiley & Sons, Inc., New York, 1999); each of which is incorporated herein by reference. The modified protein is expressed and tested. In certain embodiments, a series of variants is prepared and each variant is tested to determine its biological activity and its stability. The variant chosen for subsequent use may be the most stable one, the most active one, or the one with the greatest overall combination of activity and stability. After a first set of variants is prepared an additional set of variants may be prepared based on what is learned from the first set. The variants are typically created and overexpressed using recombinant techniques known in the art.

The inventive system has been used to create variants of GFP. These variants have been shown to be more stable and to retain their fluorescence. A GFP from *Aequorea victoria* is described in GenBank Accession Number P42212, incorporated herein by reference. The amino acid sequence of this wild type GFP is as follows:

(SEQ ID NO: 1)  
 MSKGEELFTGVVPIILVELDGDVNGHKFSVSGEGEGDATYKLTCLKFICTT  
 GKLPVPWPVLTVTTFSYGVQCFSRYPDHMKQHDFFKSAMPEGVYQERTIFF  
 KDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNV  
 YIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHY  
 LSTQSALS KDPNEKRDHMLLEFVTAAGITHGMDELYK

Wild type GFP has a theoretical net charge of -7. Using the inventive system, variants with a theoretical net charge of -29, -30, -25, +36, +48, and +49 have been created. Even after heating the +36 GFP to 95° C., 100% of the variant protein is soluble and the protein retains ≥70% of its fluorescence.

The amino acid sequences of the variants of GFP that have been created include:

GFP-NEG25  
 (SEQ ID NO: 2)  
 MGHHHHHHGASKGEELFTGVVPIILVELDGDVNGHEFVSVRGEGEGDATEG  
 ELTLKFICTTGELPVPWPVLTVTTLTYSYGVQCFSRYPDHMKQHDFFKSAMPE

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GYVQERTISFKDDGTYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHK  
 LEYNFNSHDVYITADKQENGIKAEFEIRHNVEDGSVQLADHYQQNTPIGD  
 GPVLLPDDHYLSTESALSKDPNEDRDHMLLEFVTAAGIDHGMDELYK  
 GFP-NEG29  
 (SEQ ID NO: 3)  
 MGHHHHHHGGASKGEELPDGEVPIILVELDGDVNGHEFSVRGEGEGDATEG  
 ELTLKFICTTGELPVPWPPTLVTTLTYGVCFSRYPDHMDQHDFKFSAMPE  
 GYVQERTISFKDDGTYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHK  
 LEYNFNSHDVYITADKQENGIKAEFEIRHNVEDGSVQLADHYQQNTPIGD  
 GPVLLPDDHYLSTESALSKDPNEDRDHMLLEFVTAAGIDHGMDELYK  
 GFP-NEG30  
 (SEQ ID NO: 4)  
 MGHHHHHHGGASKGEELPDGVVPIILVELDGDVNGHEFSVRGEGEGDATEG  
 ELTLKFICTTGELPVPWPPTLVTTLTYGVCFSRYPDHMDQHDFKFSAMPE  
 GYVQERTISFKDDGTYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHK  
 LEYNFNSHDVYITADKQENGIKAEFEIRHNVEDGSVQLADHYQQNTPIGD  
 GPVLLPDDHYLSTESALSKDPNEDRDHMLLEFVTAAGIDHGMDELYK  
 GFP-POS36)  
 (SEQ ID NO: 5)  
 MGHHHHHHGGASKGERLFRGKVPILVELKGDVNGHKFSVRGKGKGDATRG  
 KLTLKFICTTGKLPVPWPPTLVTTLTYGVCFSRYPKHMKRHDFFKSAMPK  
 GYVQERTISFKDKGKYKTRAEVKFEGRTLNVNRIKLKGRDFKEKGNILGHK  
 LRYNFNSHKVYITADKRNKGIKAKFKIRHNVDGSGVQLADHYQQNTPIGR  
 GPVLLPRNHYLSTRSKLSKDPKEKRDHMLLEFVTAAGIKHGRDERYK  
 GFP-POS42  
 (SEQ ID NO: 6)  
 MGHHHHHHGGRSKGRKRLFRGKVPILVELKGDVNGHKFSVRGKGKGDATRG  
 KLTLKFICTTGKLPVPWPPTLVTTLTYGVCFSRYPKHMKRHDFFKSAMPK  
 GYVQERTISFKDKGKYKTRAEVKFEGRTLNVNRIKLKGRDFKEKGNILGHK  
 LRYNFNSHKVYITADKRNKGIKAKFKIRHNVDGSGVQLADHYQQNTPIGR  
 GPVLLPRKHLYLSTRSKLSKDPKEKRDHMLLEFVTAAGIKHGRKERYK  
 GFP-POS49  
 (SEQ ID NO: 7)  
 MGHHHHHHGGRSKGRKRLFRGKVPILVCLKGDVNGHKFSVRGKGKGDATRG  
 KLTLKFICTTGKLPVPWPPTLVTTLTYGVCFSRYPKHMKRHDFFKSAMPK  
 GYVQERTISFKDKGKYKTRAEVKFKGRTLNVNRIKLKGRDFKEKGNILGHK  
 LRYNFNSHKVYITADKRNKGIKAKFKIRHNVDGSGVQLAKHYQQNTPIGR  
 GPVLLPRKHLYLSTRSKLSKDPKEKRDHMLKEFVTAAGIKHGRKERYK

As would be appreciated by one of skill in the art, homologous proteins are also considered to be within the scope of this invention. For example, any protein that includes a stretch of 20, 30, 40, 50, or 100 amino acids which are 60%, 70%, 80%, 90%, 95%, or 100% homologous to any of the above sequences is considered part of the invention. In addition, addition and deletion variants are also contemplated by the invention. In certain embodiments, any GFP with a mutated residue as shown in any of the above sequences is considered part of the invention. In certain

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Any DNA sequence that encodes the above GFP variants is also include within the scope of the invention. Exemplary DNA sequences which encode each of the variants above are as follows:

GFP-NEG25  
 (SEQ ID NO: 8)  
 ATGGGGCATCACCATCATCATCATGGCGGTGCGTCTAAGGGGGAGGAGTT  
 ATTTACGGGTGTGGTGCCGATCCTGGTGGAGCTTGATGGCGATGTTAACG  
 GCCATGAATTTTCTGTCCGCGGTGAAGGGGAGGGTGATGCCACGGAAGGG  
 GAGCTGACACTTAAATTTATTTGCACCACCGGTGAACCTCCCGTCCCGTG  
 GCCGACCTGGTGACCACCTGACCTACGCGTTCAATGCTTTTCACGTT  
 ATCCGGATCACATGAAGCAACACGACTTCTTTAAAGCGCGATGCCTGAA  
 GGCTATGTTCAAGAACGTACAATTAGTTTAAAGATGACGGCACCTACAA  
 GACCGTGCGGAAGTAAATTTGAAGGGGACACTTTAGTGAACCGCATCG  
 AGCTGAAAGGGATCGATTTTAAAGAAGATGGGAATATCCTGGGACACAAA  
 CTTGAATACAACTTAAATAGTCATGACGTCTATATCACGGCGGACAAACA  
 GGAAACCGAATTAAGGCAGAATTTGAGATTCCGCATAATGTCGAAGATG  
 GCTCCGTACAGTTGGCTGATCACTATCAGCAGAATACGCCGATTGGAGAT  
 GGTCGGTTTTATTACCAGACGATCACTATCTGTCCACCGAATCCGCCCT  
 GAGCAAAGATCCGAATGAAGACCGGGACCATATGGTTCTGCTGGAATTTG  
 TTACGGCGGCTGGTATTGACCATGGCATGGATGAGCTGTATAAGTAG  
 GFP-NEG29  
 (SEQ ID NO: 9)  
 ATGGGGCATCACCATCATCATCATGGCGGTGCGTCTAAGGGGGAGGAGTT  
 ATTTGATGGTGAAGTGCCGATCCTGGTGGAGCTTGATGGCGATGTTAACG  
 GCCATGAATTTTCTGTCCGCGGTGAAGGGGAGGGTGATGCCACGGAAGGG  
 GAGCTGACACTTAAATTTATTTGCACCACCGGTGAACCTCCCGTCCCGTG  
 GCCGACCTGGTGACCACCTGACCTACGCGTTCAATGCTTTTCACGTT  
 ATCCGGATCACATGGACCAACACGACTTCTTTAAAGCGCGATGCCTGAA  
 GGCTATGTTCAAGAACGTACAATTAGTTTAAAGATGACGGCACCTACAA  
 GACCGTGCGGAAGTAAATTTGAAGGGGACACTTTAGTGAACCGCATCG  
 AGCTGAAAGGGATCGATTTTAAAGAAGATGGGAATATCCTGGGACACAAA  
 CTTGAATACAACTTAAATAGTCATGACGTCTATATCACGGCGGACAAACA  
 GGAAACCGAATTAAGGCAGAATTTGAGATTCCGCATAATGTCGAAGATG  
 GCTCCGTACAGTTGGCTGATCACTATCAGCAGAATACGCCGATTGGAGAT  
 GGTCCGGTTTTATTACCAGACGATCACTATCTGTCCACCGAATCCGCCCT  
 GAGCAAAGATCCGAATGAAGACCGGGACCATATGGTTCTGCTGGAATTTG  
 TTACGGCGGCTGGTATTGACCATGGCATGGATGAGCTGTATAAGTAG  
 GFP-NEG30  
 (SEQ ID NO: 10)  
 ATGGGGCATCACCATCATCATCATGGCGGTGCGTCTAAGGGGGAGGAGTT  
 ATTTGATGGTGTGGTGCCGATCCTGGTGGAGCTTGATGGCGATGTTAACG  
 GCCATGAATTTTCTGTCCGCGGTGAAGGGGAGGGTGATGCCACGGAAGGG  
 GAGCTGACACTTAAATTTATTTGCACCACCGGTGAACCTCCCGTCCCGTG  
 GCCGACCTGGTGACCACCTGACCTACGCGTTCAATGCTTTTCAGATT

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ATCCGGATCACATGGACCAACACGACTTCTTTAAAGCGCGATGCCTGAA  
 GGCTATGTTCAAGAACGTACAATTAGTTTTAAAGATGACGGCACCTACAA  
 GACCCGTGCGGAAGTAAATTTGAAGGGGACACTTTAGTGAACCGCATCG  
 AGCTGAAAGGGATCGATTTTAAAGAAGATGGGAATATCTGGGACACAAA  
 CTGGAATACAACTTTAATAGTCATGACGTCTATATCACGGCGGACAAA  
 GGAAACCGAATTAAAGCAGAATTTGAGATTCGGCATAATGTCGAAGATG  
 GCTCGGTACAGTTGGCTGATCACTATCAGCAGAATACGCCGATTGGAGAT  
 GGTCCGGTTTTATTACCAGACGATCACTATCTGTCCACCGAATCCGCCCT  
 GAGCAAAGATCCGAATGAAGACCGGGACCATATGGTTCTGTGGAATTTG  
 TTACGGCGCGTGGTATTGACCATGGCATGGATGAGCTGTATAAGTAG  
 GFP-POS36  
 (SEQ ID NO: 11)  
 ATGGGCGATCATCATCATCACACGGCGGGCGTCTAAGGGAGAGCGCTT  
 GTTTCGCGGCAAGTCCCGATTCTTGTGGAGCTCAAAGGTGATGTAAATG  
 GTCATAAATTTAGTGTGCGCGGAAAGGAAAGGAGATGCTACGCGGGGC  
 AAGCTCACCTGAAATTTATTGCAACAACCGGCAAACTGCCAGTCCCGTG  
 GCCTACATTAGTCACTACTCTGACGTACGGTGTTCAGTGCTTTTCTCGCT  
 ATCCCAAACACATGAAACGCCATGATTTCTTCAAGAGCGCGATGCCAAAA  
 GGTATGTGTCAGGAACGCACCATCAGCTTTAAAAAGACGGCAATATAA  
 AACCCTGTCAGAAGTTAAATTCGAAGGCGCACCTGGTCAACCGCATT  
 AACTGAAAGGTCTGTGACTTCAAAGGAAAGGTAATATTCTTGGTCACAAA  
 CTGCGCTATAATTTCAACTCTCACAAGTTTATATTACGGCGGATAAACG  
 TAAAAACGGGATTAAAGCGAATTTAAGATTCTGCATAATGTTAAAGACG  
 GCAGTGTGCAGTTAGCGGATCATTTATCAGCAGAATACCCCAATTGGTCGC  
 GGTCCAGTGTCTGCCCGTAACCATTTATCTGTGACCCCGCAGCAAACT  
 CAGCAAGACCCGAAAGAAAAACGTGACCACATGTTACTGGAATTTG  
 TGACCGCAGCAGGCATTAAACATGGCCGCGATGAACGTTACAAATAG  
 GFP-POS42  
 (SEQ ID NO: 12)  
 ATGGGCCATCATCATCACACACGGCGGCCGCTCAAAGGTAAACGCTT  
 GTTCCGTGGTAAAGTACCGATCTTAGTGGAGCTCAAAGGGGATGTGAATG  
 GCCATAAGTTCTCGGTTCTGTGGCAAAGGTAAGGGAGATGCGACGCGCGGC  
 AAATTAACGCTGAAATTCATTGTACTACAGGTAAACTGCCGGTGCCATG  
 GCCTACTCTCGTCACCACGTTGACCTATGGGGTTCAATGCTTCAGCCGGT  
 ACCCTAAACACATGAAGCGCCACGATTCTTCAAATCGCGATGCCAAAG  
 GGGTATGTCCAGGAACGCATATCAGCTTCAAAAAGACGGTAAGTATAA  
 AACTCGTGCTGAAGTTAAATTCGAAGGACGCACACTGGTAAATCGCATT  
 AATTGAAGGGGCGGACTTTAAGGAAAAAGGTAATATCTTAGGTCACAAA  
 TTGCGCTACAACCTCAACTCTCATAAAGTTTACATTACAGCAGATAAGCG  
 TAAAAATGGCATCAAAGCGAATTCAAAATTCGTACCAATGTGAAAGATG  
 GTAGCGTGCAATTAGCCGATCATACCAGCAGAATACGCCGATCGGTGCG  
 GGCCAGTACTGTTGCGCGCAACATTACTTATCTACCCGAGTAAACT

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GTCTAAAGACCCAAAGAGAAGCGCGACCATATGGTTCTCTGGAGTTTG  
 TCACCGCCCGCGAATTAAACACGGCCGCAAGAGCGCTATAAATAG  
 5 GFP-POS49  
 (SEQ ID NO: 13)  
 ATGGGCCACCATCATCATCACACGGGGACGCTCTAAAGGTAAACGCTCT  
 GTTTCGTGGAAAGGTGCCCATCTCTGGTTAAACTCAAAGGTGATGTCAACG  
 10 GCCATAAGTTTTCGGTTCGTGGCAAAGGTAAAGGTGATGCGACGCGCGGG  
 AAATTAACACTGAAATTTATTGCAACAACCGGAAAACTCCCTGTGCCGTG  
 15 GCCGACTTTGGTGACCACATTAACCTATGGTGTTCATGCTTCTCACGTT  
 ATCCGAAGCATATGAAACGTATGATTTTTTCAAATCGGTATGCCGAA  
 GGTTACGTCCAGGAGCGCACCATCTCATTTAAGAAAGACGGTAAGTATAA  
 20 AACCCTGCTGAAGTAAATTCGAAGGACGCACCTGGTGAATCGCATT  
 AACTGAAAGGTCTGTGATTTCAAAGAAAAGGGAATATTTTAGGGCATAAG  
 CTCCGTTATAATTTTAAACAGTCATAAGGTGTATATTACCGTGATAAACG  
 25 CAAAAACGGAATCAAAGCGAATTTAAGATCCGTACATGTAAAGATG  
 GCTCAGTCCAACCTGGCAAACATTACCAGCAGAATACCCCGATCGGCCGC  
 30 GGTCTGTGCTTCTGCGCGTAAACACTACTTGTGCGACCCGGTCAAAT  
 GAGTAAAGATCCGAAGGAAAAGCGTGATCACATGGTCTTGAAGGAATTTG  
 TAATGCGAGCAGGTATTAAACACGGGCGCAAAGAACGTTACAAATAG  
 35

Polynucleotide sequence homologous to the above sequences are also within the scope of the present invention. In certain embodiments, the polynucleotide sequence include a stretch of 50, 100, or 150 nucleotides that are 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% homologous to any one of the above sequence. The present invention also includes sequence where one or more nucleotides is inserted or deleted from one of the above sequences. Any polynucleotide sequence with a mutation as shown in any of the sequences above is considered part of the invention. In certain embodiments, the sequence includes 2, 3, 4, 5, 6, 7, 8, 9, 10, or more mutations as shown in any of the sequences above.

The present invention also provides vector (e.g., plasmids, cosmid, viruses, etc.) that comprise any of the inventive sequences herein or any other sequence (DNA or protein) modified using the inventive system. In certain embodiments, the vector includes elements such as promoter, enhancer, ribosomal binding sites, etc. sequences useful in overexpressing the inventive GFP variant in a cell. The invention also includes cells comprising the inventive sequences or vectors. In certain embodiments, the cells overexpress the variant GFP. The cells may be bacterial cells (e.g., *E. coli*), fungal cells (e.g., *P. pastoris*), yeast cells (e.g., *S. cerevisiae*), mammalian cells (e.g., CHO cells), or human cells.

The inventive system has been used to create variants of streptavidin. These variants have been shown to form soluble tetramers that bind biotin. The amino acid sequence of this wild type streptavidin is as follows:

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(SEQ ID NO: 28)  
AAEAGITGTWYNQLGSTFIVTAGADGALTGTYESAVGNAESRYVLTGRYD  
SAPATDGS GTALGWTVAWKNNYRNAHSATTWSGQYVGGAEARINTQWLLT  
SGTTEANAWKSTLVGHDTFTKVKPSAAS

Wild type streptavidin has a theoretical net charge of -4. Using the inventive system, variants with a theoretical net charge of -40 and +52 have been created. Even after heating the variants to 100° C., the proteins remained soluble.

The amino acid sequences of the variants of streptavidin that have been created include:

SAV-NEG40  
(SEQ ID NO: 29)  
MGHHHHHHGGAEAGITGTWYNQLGSTFIVTAGADGALTGTYESAVGDAES  
EYVLTGRYDSAPATDGS GTALGWTVAWKNDYENHSATTWSGQYVGGAEA  
RINTQWLLTSGTTEADAWKSTLVGHDTFTKVEPSAAS

SAV-POS52  
(SEQ ID NO: 30)  
MGHHHHHHGGAKAGITGTWYNQLGSTFIVTAGAKGALTGTYESAVGNAKS  
RYVLTGRYDSAPATKGSGTALGWTVAWKNNYRNAHSATTWSGQYVGGAKA  
RINTQWLLTSGTTKAKAWKSTLVGHDTFTKVKPSAAS

As would be appreciated by one of skill in the art, homologous proteins are also considered to be within the scope of this invention. For example, any protein that includes a stretch of 20, 30, 40, 50, or 100 amino acids which are 60%, 70%, 80%, 90%, 95%, or 100% homologous to any of the above sequences is considered part of the invention. In addition, addition and deletion variants are also contemplated by the invention. In certain embodiments, any streptavidin with a mutated residue as shown in any of the above sequences is considered part of the invention. In certain embodiments, the sequence includes 2, 3, 4, 5, 6, 7, 8, 9, 10, or more mutations as shown in any of the sequences above.

Any DNA sequence that encodes the above streptavidin variants is also included within the scope of the invention. Exemplary DNA sequences which encode each of the variants above are as follows:

SAV-NEG40  
(SEQ ID NO: 31)  
GGTTCAGCCATGGGTATCACCACCACCATCACGGTGGCGCCGAAGCAGG  
TATTACCGGTACCTGGTATAACCAAGTTAGGCTCAACCTTTATTGTGACCG  
CGGGAGCGGACGGCGCCTTAACCGGTACCTACGAATCAGCTGTAGGTGAC  
GCGGAATCAGAGTACGTATTAACCGGTGTTATGATAGCGCGCCGGCGAC  
TGACGGTAGCGGTACTGCTTTAGGTTGGACCGTAGCGTGGAAGAATGATT  
ATGAAACGCACATAGCGCAACAACGTGGTACGGCAGTACGTTGGCGGA  
GCTGAGGCGCGCATTAACACGAGTGGTTATTAAGTAGCGGCACCACTGA  
AGCTGATGCTTGAAGAGCAGCTTAGTGGGTCATGATACCTTCACTAAAG  
TGAACCTTACAGTGCCTCATAATAATGACTCGAGACCTGCA

SAV-POS52  
(SEQ ID NO: 32)  
GGTTCAGCCATGGGTATCACCACCACCATCACGGTGGCGCCGAAGCAGG  
TATTACCGGTACCTGGTATAACCAAGTTAGGCTCAACCTTTATTGTGACCG

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-continued

CGGGAGCGAAAGGCGCCTTAACCGGTACCTACGAATCAGCTGTAGGAAAC  
GCAAAATCACGCTACGTATTAACCGGTGTTATGATAGCGCGCCGGCGAC  
TAAAGGTAGCGGTACTGCTTTAGGTTGGACCGTAGCGTGGAAGAATAAGT  
ATCGTAATGCGCACAGTGCTACCACTTGGTCAGGGCAGTACGTAGGGGGA  
GCCAAAGCACGTATCAACACGAGTGGTTATTAACATCAGGTACCACCAA  
AGCGAAAGCCTGGAAGAGCACGTTAGTGGGTCATGATACCTTCACTAAAG  
TGAAACCTTACAGTGCCTCATAATAATGACTCGAGACCTGCA

Polynucleotide sequence homologous to the above sequences are also within the scope of the present invention. In certain embodiments, the polynucleotide sequence include a stretch of 50, 100, or 150 nucleotides that are 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% homologous to any one of the above sequence. The present invention also includes sequence where one or more nucleotides is inserted or deleted from one of the above sequences. Any polynucleotide sequence with a mutation as shown in any of the sequences above is considered part of the invention. In certain embodiments, the sequence includes 2, 3, 4, 5, 6, 7, 8, 9, 10, or more mutations as shown in any of the sequences above.

The present invention also provides vector (e.g., plasmids, cosmids, viruses, etc.) that comprise any of the inventive sequences herein or any other sequence (DNA or protein) modified using the inventive system. In certain embodiments, the vector includes elements such as promoter, enhancer, ribosomal binding sites, etc. sequences useful in overexpressing the inventive streptavidin variant in a cell. The invention also includes cells comprising the inventive sequences or vectors. In certain embodiments, the cells overexpress the variant streptavidin. The cells may be bacterial cells (e.g., *E. coli*), fungal cells (e.g., *P. pastoris*), yeast cells (e.g., *S. cerevisiae*), mammalian cells (e.g., CHO cells), or human cells.

The inventive system has been used to created variants of glutathione-S-transferase (GST). These variants have been shown to retain the catalytic activity of wild type GST. The amino acid sequence of this wild type GST is as follows:

(SEQ ID NO: 33)  
MGHHHHHHGGPPYITITYFPVGRCEAMRMLADQDSWKEEVVMTETWPP  
LKPSCLFRQLPKFQDGLTLYQSNAILRLHGRSFGLYGKDQKEAALVDMV  
NDGVEDLRCKYATLIYTNIEAGKEYVKELPEHLKPFETLLSQNGGQAF  
VVGSIQSFADYNLLDLLRIHQVLNPSCLDAPFLLSAYVARLSARPKIKAF  
LASPEHVNRPINGNGKQ

Wild type GST has a theoretical net charge of +2. Using the inventive system, a variant with a theoretical net charge of -40 has been created. This variant catalyzes the addition of glutathione to chloronitrobenzene with a specific activity only 2.7-fold lower than that of wild type GST. Even after heating the variant to 100° C., the protein remained soluble, and the protein recovered 40% of its catalytic activity upon cooling.

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The amino acid sequences of variants of GST include:

GST-NEG40 (SEQ ID NO: 34)  
 MGHHHHHHGGPPYITITYFPVRGRCEAMRMLLADQDQSWEEVVTMETWPP  
 LKPSCLFRQLPKFQDGLTLYQSNAILRHLGRSFLYGEDEEEAALVDMV  
 NDGVEDLRCKYATLIYTDYEAGKEEYVEELPEHLKPFETLLSENEGGEAF  
 VVGSEISFADYNLLDLRLHQVLNPSCLDAFPLLSAYVARLSARPEIEAF  
 LASPEHVDRLPINGNGKQ  
 GST-POS50 (SEQ ID NO: 35)  
 MGHHHHHHGGPPYITITYFPVRGRCEAMRMLLADQKQSWKEEVVTMTWPP  
 LKPSCLFRQLPKFQDGLTLYQSNAILRHLGRSFLYGKKQKEAALVDMV  
 NDGVEDLRCKYATLIYTKYKAGKKYVKKLPKHLKPFETLLSKNKGKAF  
 VVGSKI SFADYNLLDLRLHQVLNPSCLKAFPLLSAYVARLSARPKIKAF  
 LASPEHVKRPINGNGKQ

As would be appreciated by one of skill in the art, homologous proteins are also considered to be within the scope of this invention. For example, any protein that includes a stretch of 20, 30, 40, 50, or 100 amino acids which are 60%, 70%, 80%, 90%, 95%, or 100% homologous to any of the above sequences is considered part of the invention. In addition, addition and deletion variants are also contemplated by the invention. In certain embodiments, any streptavidin with a mutated residue as shown in any of the above sequences is considered part of the invention. In certain embodiments, the sequence includes 2, 3, 4, 5, 6, 7, 8, 9, 10, or more mutations as shown in any of the sequences above.

Any DNA sequence that encodes the above GST variants is also included within the scope of the invention. Exemplary DNA sequences which encode each of the variants above are as follows:

GST-NEG40 (SEQ ID NO: 36)  
 GGTT CAGCCATGGGT CATCACCACCACCAT CACGGTGGCCCGCGTACAC  
 CATTACATACTTTCCGGTACGTGGTCGTTGTGAAGCGATGCGTATGTTAT  
 TAGCGGACCAGGACCAATCATGGGAAGAAGAAGTAGTGACAATGGAAACC  
 TGGCCCGCGTTAAAGCCTAGCTGTTTATTCGGTCAATTACCGAAGTTTCA  
 GGATGGTGATTTAACTTTATACCAGTCTAACGCGATCTTACGTCATTTAG  
 GTCGCTCATTGGTTTATACGGTGAAGATGAAGAAGAAGCAGCCTTAGTG  
 GATATGGTGAATGATGGCGTGAAGACTTACGTTGTAAATACGCGACGTT  
 AATTTACTACTGATTATGAAGCCGGTAAAGAGGAGTACGTGAAGAATTAC  
 CTGAACACCTGAAGCCGTTTGAACATTACTGAGCGAAAAATGAAGGAGGT  
 GAGGCGTTTCGTAGTTGGTAGCGAAATTAGCTTCGCTGATTATAACTTATT  
 AGACTTATTACGATTACACAGGTTTTAAATCCTAGCTGTTTAGACGCTT  
 TCCCGTTACTGAGCGCATATGTAGCGCGCTGAGCGCCCGTCCGGAATT  
 GAAGCTTTCTTAGCGTCACCTGAACACGTAGACCGCCCGATTAAACGGAAA  
 CGGAAGCAGTAATAATGAGGTACCACTGCA  
 GST-POS50 (SEQ ID NO: 37)

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-continued

GGTT CAGCCATGGGT CATCACCACCACCAT CACGGTGGCCCGCGTACAC  
 CATTACATACTTTCCGGTACGTGGTCGTTGTGAAGCGATGCGTATGTTAT  
 5 TAGCGGACCAGAAACAATCATGGAAAGAAGAAGTAGTGACAATGAAGACC  
 TGGCCCGCGTTAAAGCCTAGCTGTTTATTCGGTCAATTACCGAAGTTTCA  
 GGATGGTAAATTAACCTTATACCAGTCTAACGCGATCTTACGTCATTTAG  
 10 GTCGCTCATTGGTTTATACGGTAAGAAGCAGAAAGAAGCAGCCTTAGTG  
 GATATGGTGAATGATGGCGTGAAGACTTACGTTGTAAATACGCGACGTT  
 AATTTACTACTAAATATAAGCCGGTAAAAAGAAGTACGTGAAAAATTAC  
 15 CTAAACACCTGAAGCCGTTTGAACATTACTGAGCAAAAAATGAAGGAGGT  
 AAGGCGTTTCGTAGTTGGTAGCAAGATTAGCTTCGCTGATTATAACTTATT  
 AGACTTATTACGATTACACAGGTTTTAAATCCTAGCTGTTTAAAGGCTT  
 20 TCCCGTTACTGAGCGCATATGTAGCGCGCTGAGCGCCCGTCCGGAATC  
 AAAGCTTTCTTAGCGTCACCTGAACACGTGAAGCGCCCGATTAAACGGAAA  
 CGGCAAGCAGTAATAATGAGGTACCACTGCA

The present invention also provides vector (e.g., plasmids, cosmids, viruses, etc.) that comprise any of the inventive sequences herein or any other sequence (DNA or protein) modified using the inventive system. In certain embodiments, the vector includes elements such as promoter, enhancer, ribosomal binding sites, etc. sequences useful in overexpressing the inventive GST variant in a cell. The invention also includes cells comprising the inventive sequences or vectors. In certain embodiments, the cells overexpress the variant GST. The cells may be bacterial cells (e.g., *E. coli*), fungal cells (e.g., *P. pastoris*), yeast cells (e.g., *S. cerevisiae*), mammalian cells (e.g., CHO cells), or human cells.

The present invention also includes kits for modifying proteins of interest to produce more stable variants of the protein. These kits typically include all or most of the reagents needed create a more stable variant of a protein. In certain embodiments, the kit includes computer software to aid a researcher in designing the more stable variant protein based on the inventive method. The kit may also include all of some of the following: reagents, primers, oligonucleotides, nucleotides, enzymes, buffers, cells, media, plates, tubes, instructions, vectors, etc. The research using the kit typically provides the DNA sequence for mutating to create the more stable variant. The contents are typically packaged for convenience use in a laboratory.

These and other aspects of the present invention will be further appreciated upon consideration of the following Examples, which are intended to illustrate certain particular embodiments of the invention but are not intended to limit its scope, as defined by the claims.

## EXAMPLES

### Example 1

#### Supercharging Proteins can Impart Extraordinary Resilience

Protein aggregation, a well known culprit in human disease (Cohen, F. E.; Kelly, J. W., *Nature* 2003, 426, (6968), 905-9; Chiti, F.; Dobson, C. M., *Annu Rev Biochem* 2006, 75, 333-66; each of which is incorporated herein by reference), is also a major problem facing the use of proteins as therapeutic or diagnostic agents (Frokjaer, S.; Otzen, D. E.,

*Nat Rev Drug Discov* 2005, 4, (4), 298-306; Fowler, S. B.; Poon, S.; Muff, R.; Chiti, F.; Dobson, C. M.; Zurdo, J., *Proc Natl Acad Sci USA* 2005, 102, (29), 10105-10; each of which is incorporated herein by reference). Insights into the protein aggregation problem have been garnered from the study of natural proteins. It has been known for some time that proteins are least soluble at their isoelectric point, where they bear a net charge of zero (Loeb, J., *J Gen Physiol* 1921, 4, 547-555; incorporated herein by reference). More recently, small differences in net charge ( $\pm 3$  charge units) have been shown to predict aggregation tendencies among variants of a globular protein (Chiti, F.; Stefani, M.; Taddei, N.; Ramponi, G.; Dobson, C. M., *Nature* 2003, 424, (6950), 805-8; incorporated herein by reference), and also among intrinsically disordered peptides (Pawar, A. P.; Dubay, K. F.; Zurdo, J.; Chiti, F.; Vendruscolo, M.; Dobson, C. M., *J Mol Biol* 2005, 350, (2), 379-92; incorporated herein by reference). Together with recent evidence that some proteins can tolerate significant changes in net charge (for example, the finding that carbonic anhydrase retains catalytic activity after exhaustive chemical acetylation of its surface lysines (Gudiksen et al., *J Am Chem Soc* 2005, 127, (13), 4707-14; incorporated herein by reference)), these observations led us to conclude that the solubility and aggregation resistance of some proteins might be significantly enhanced, without abolishing their folding or function, by extensively mutating their surfaces to dramatically increase their net charge, a process we refer to herein as "supercharging".

We began with a recently reported state-of-the-art variant of green fluorescent protein (GFP) called "superfolder GFP" (sfGFP), which has been highly optimized for folding efficiency and resistance to denaturants (Pedelacq et al., *Nat Biotechnol* 2006, 24, (1), 79-88; incorporated herein by reference). Superfolder GFP has a net charge of  $-7$ , similar to that of wild-type GFP. Guided by a simple algorithm to calculate solvent exposure of amino acids (see Materials and Methods), we designed a supercharged variant of GFP having a theoretical net charge of  $+36$  by mutating 29 of its most solvent-exposed residues to positively charged amino acids (FIG. 1). The expression of genes encoding either sfGFP or GFP( $+36$ ) yielded intensely green-fluorescent bacteria. Following protein purification, the fluorescence properties of GFP( $+36$ ) were measured and found to be very similar to those of sfGFP. Encouraged by this finding, we designed and purified additional supercharged GFPs having net charges of  $+48$ ,  $-25$ , and  $-30$ , all of which were also found to exhibit sfGFP-like fluorescence (FIG. 2a). All supercharged GFP variants showed circular dichroism spectra similar to that of sfGFP, indicating that the proteins have similar secondary structure content (FIG. 2b). The thermodynamic stabilities of the supercharged GFP variants were only modestly lower than that of sfGFP (1.0-4.1 kcal/mol, FIG. 2c and Table 1) despite the presence of as many as 36 mutations.

Although sfGFP is the product of a long history of GFP optimization (Giepmans et al., *Science* 2006, 312, (5771), 217-24; incorporated herein by reference), it remains susceptible to aggregation induced by thermal or chemical unfolding. Heating sfGFP to  $100^\circ\text{C}$ . induced its quantitative precipitation and the irreversible loss of fluorescence (FIG. 3a). In contrast, supercharged GFP( $+36$ ) and GFP( $-30$ ) remained soluble when heated to  $100^\circ\text{C}$ ., and recovered significant fluorescence upon cooling (FIG. 3a). Importantly, while 40% 2,2,2-trifluoroethanol (TFE) induced the complete aggregation of sfGFP at  $25^\circ\text{C}$ . within minutes, the  $+36$  and  $-30$  supercharged GFP variants suffered no significant aggregation or loss of fluorescence under the same conditions for hours (FIG. 3b).

In addition to this remarkable aggregation resistance, supercharged GFP variants show a strong, reversible avidity

for highly charged macromolecules of the opposite charge (FIG. 3c). When mixed together in 1:1 stoichiometry, GFP( $+36$ ) and GFP( $-30$ ) immediately formed a green fluorescent co-precipitate, indicating the association of folded proteins. GFP( $+36$ ) similarly co-precipitated with high concentrations of RNA or DNA. The addition of NaCl was sufficient to dissolve these complexes, consistent with the electrostatic basis of their formation. In contrast, sfGFP was unaffected by the addition of GFP( $-30$ ), RNA, or DNA (FIG. 3c).

We next sought to determine whether the supercharging principle could apply to proteins other than GFP, which is monomeric and has a well-shielded fluorophore. To this end, we applied the supercharging process to two proteins unrelated to GFP. Streptavidin is a tetramer with a total net charge of  $-4$ . Using the solvent-exposure algorithm, we designed two supercharged streptavidin variants with net charges of  $-40$  or  $+52$ . Both supercharged streptavidin variants were capable of forming soluble tetramers that bind biotin, albeit with reduced affinity.

Glutathione-S-transferase (GST), a dimer with a total net charge of  $+2$ , was supercharged to yield a dimer with net charge of  $-40$  that catalyzed the addition of glutathione to chlorodinitrobenzene with a specific activity only 2.7-fold lower than that of wild-type GST (FIG. 3d). Moreover, the supercharged streptavidins and supercharged GST remained soluble when heated to  $100^\circ\text{C}$ ., in contrast to their wild-type counterparts, which, like sfGFP, precipitated quantitatively and irreversibly (Table 1). In addition, GST( $-40$ ) recovered 40% of its catalytic activity upon cooling (FIG. 3d).

In summary, we have demonstrated that monomeric and multimeric proteins of varying structures and functions can be "supercharged" by simply replacing their most solvent-exposed residues with like-charged amino acids. Supercharging profoundly alters the intermolecular properties of proteins, imparting remarkable aggregation resistance and the ability to associate in folded form with oppositely charged macromolecules like "molecular Velcro." We note that these unusual intermolecular properties arise from high net charge, rather than from the total number of charged amino acids, which was not significantly changed by the supercharging process (Table 1).

In contrast to these dramatic intermolecular effects, the intramolecular properties of the seven supercharged proteins studied here, including folding, fluorescence, ligand binding, and enzymatic catalysis, remained largely intact. Supercharging therefore may represent a useful approach for reducing the aggregation tendency and improving the solubility of proteins without abolishing their function. These principles may be particularly useful in de novo protein design efforts, where unpredictable protein handling properties including aggregation remain a significant challenge. In light of the above results of supercharging natural proteins, it is tempting to speculate that the aggregation resistance of designed proteins could also be improved by biasing the design process to increase the frequency of like-charged amino acids at positions predicted to lie on the outside of the folded protein.

Protein supercharging illustrates the remarkable plasticity of protein surfaces and highlights the opportunities that arise from the mutational tolerance of solvent-exposed residues. For example, it was recently shown that the thermodynamic stability of some proteins can be enhanced by rationally engineering charge-charge interactions (Strickler et al., *Biochemistry* 2006, 45, (9), 2761-6; incorporated herein by reference). Protein supercharging demonstrates how this plasticity can be exploited in a different way to impart extraordinary resistance to protein aggregation. Our findings are consistent with the results of a complementary study in which removal of all charges from ubiquitin left its folding



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intact but significantly impaired its solubility (Loladze et al, *Protein Sci* 2002, 11, (1), 174-7; incorporated herein by reference).

These observations may also illuminate the modest net-charge distribution of natural proteins (Knight et al., *Proc Natl Acad Sci USA* 2004, 101, (22), 8390-5; Gitlin et al., *Angew Chem Int Ed Engl* 2006, 45, (19), 3022-60; each of which is incorporated herein by reference): the net charge of 84% of Protein Data Bank (PDB) polypeptides, for example, falls within  $\pm 10$ . Our results argue against the hypothesis that high net charge creates sufficient electrostatic repulsion to force unfolding. Indeed, GFP(+48) has a higher positive net charge than any polypeptide currently in the PDB, yet retains the ability to fold and fluoresce. Instead, our findings suggest that nonspecific intermolecular adhesions may have disfavored the evolution of too many highly charged natural proteins. Almost all natural proteins with very high net

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*Nat Biotechnol* 24, 79-88 (2006); each of which is incorporated herein by reference) as those having AvNAPSA<150, where AvNAPSA is average neighbor atoms (within 10 Å) per sidechain atom. Charged or highly polar solvent-exposed residues (DERKNQ) were mutated either to Asp or Glu, for negative-supercharging (red); or to Lys or Arg, for positive-supercharging (blue). Additional surface-exposed positions to mutate in green fluorescent protein (GFP) variants were chosen on the basis of sequence variability at these positions among GFP homologues. The supercharging design process for streptavidin (SAV) and glutathione-S-transferase (GST) was fully automated: residues were first sorted by solvent exposure, and then the most solvent-exposed charged or highly polar residues were mutated either to Lys for positive supercharging, or to Glu (unless the starting residue was Asn, in which case to Asp) for negative supercharging.

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1
SAV(-40) MGHHHHHHGGAEAGITGTWYNQLGSTFIVTAGADGALTGTYESAVGESSVLTGRYDSAPATDGGSTA
wtSAV -----AAEAGITGTWYNQLGSTFIVTAGADGALTGTYESAVGNAESRYVLTGRYDSAPATDGGSTA
SAV(+52) MGHHHHHHGGAKAGITGTWYNQLGSTFIVTAGA3ALTGTYESAVGNA3RYVLTGRYDSAPAT3SGSTA

71
SAV(-40) LGWTVAWKNYNAHSATTWSGQYVGGAEARINTQWLLTSGTTEAAWKSTLVGHDTFTKVPSAAAS
wtSAV LGWTVAWKNYNRNAHSATTWSGQYVGGAEARINTQWLLTSGTTEANAAKSTLVGHDTFTKVKPSAAAS
SAV(+52) LGWTVAWKNYRNAHSATTWSGQYVGGAKARINTQWLLTSGTTAKAKSTLVGHDTFTKVKPSAAAS

SAV(-40) (SEQ ID NO: 29); wtSAV (SEQ ID NO: 28); and SAV(+52) (SEQ ID NO: 30).

1
GST(-40) MGHHHHHHGGPPYTITYPFVRGRCEAMRMLLADQDSWEVVTMETWPPLKPSCLFRQLPKFQDGLTLYQSNA
wtGST MGHHHHHHGGPPYTITYPFVRGRCEAMRMLLADQDSWKEEVVTMETWPPLKPSCLFRQLPKFQDGLTLYQSNA
GST(+50) MGHHHHHHGGPPYTITYPFVRGRCEAMRMLLADQDSWKEEVVTMTWPPLKPSCLFRQLPKFQDG3TLYQSNA

75
GST(-40) ILRHLGRSFGLYGDEAALVDMVNDGVEDLRCKYATLIYTYEAGKEYVELPEHLKPFETLLSNGGAF
wtGST ILRHLGRSFGLYGKDQKEAALVDMVNDGVEDLRCKYATLIYTNYEAGKEYVKELEHLKPFETLLSQNGGQAF
GST(+50) ILRHLGRSFGLYGKDQKEAALVDMVNDGVEDLRCKYATLIYTYEAGKEYVK3ELKPFETLLSNGGAF

151
GST(-40) VVGSISFADYNLLDLLRIHQVLNPSCLDAFPLLSAYVARLSARP3AFLASPEHV3PPINGNGKQ
wtGST VVGSISFADYNLLDLLRIHQVLNPSCLDAFPLLSAYVARLSARPKIKAFLASPEHVNRPPINGNGKQ
GST(+50) VVGSISFADYNLLDLLRIHQVLNPSCLKAPPLLSAYVARLSARPKIKAFLASPEHV3PPINGNGKQ

GST(-40) (SEQ ID NO: 34); wtGST (SEQ ID NO: 33); and GST(+50) (SEQ ID NO: 35).

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charge, such as ribosomal proteins L3 (+36) and L15 (+44), which bind RNA, or calsequestrin (-80), which binds calcium cations, associate with oppositely charged species as part of their essential cellular functions.

#### Materials and Methods

##### Design Procedure and Supercharged Protein Sequences.

Solvent-exposed residues (shown in grey below) were identified from published structural data (Weber, P. C., Ohlendorf, D. H., Wendoloski, J. J. & Salemme, F. R. Structural origins of high-affinity biotin binding to streptavidin. *Science* 243, 85-88 (1989); Dirr, H., Reinemer, P. & Huber, R. Refined crystal structure of porcine class Pi glutathione S-transferase (pGST P1-1) at 2.1 Å resolution. *J Mol Biol* 243, 72-92 (1994); Pedelacq, J. D., Cabantous, S., Tran, T., Terwilliger, T. C. & Waldo, G. S. Engineering and characterization of a superfolder green fluorescent protein.

#### Protein Expression and Purification.

Synthetic genes optimized for *E. coli* codon usage were purchased from DNA 2.0, cloned into a pET expression vector (Novagen), and overexpressed in *E. coli* BL21(DE3) pLysS for 5-10 hours at 15° C. Cells were harvested by centrifugation and lysed by sonication. Proteins were purified by Ni-NTA agarose chromatography (Qiagen), buffer-exchanged into 100 mM NaCl, 50 mM potassium phosphate pH 7.5, and concentrated by ultrafiltration (Millipore). All GFP variants were purified under native conditions. Wild-type streptavidin was purchased from Promega. Supercharged streptavidin variants were purified under denaturing conditions and refolded as reported previously for wild-type streptavidin (Thompson et al. Construction and expression of a synthetic streptavidin-encoding gene in *Escherichia coli*. *Gene* 136, 243-246 (1993); incorporated herein by

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reference), as was supercharged GST. Wild-type GST was purified under either native or denaturing conditions, yielding protein of comparable activity.

Electrostatic Surface Potential Calculations (FIG. 1b).

Models of -30 and +48 supercharged GFP variants were based on the crystal structure of superfolder GFP (Pedelacq et al., Engineering and characterization of a superfolder green fluorescent protein. *Nat Biotechnol* 24, 79-88 (2006); incorporated herein by reference). Electrostatic potentials were calculated using APBS (Baker et al., Electrostatics of nanosystems: application to microtubules and the ribosome. *Proc Natl Acad Sci USA* 98, 10037-10041 (2001); incorporated herein by reference) and rendered with PyMol (Delano, W. L., The PyMOL Molecular Graphics System, www[dot]pymol[dot]org (2002); incorporated herein by reference) using a scale of -25 kT/e (red) to +25 kT/e (blue).

Protein Staining and UV-Induced Fluorescence (FIG. 2a).

0.2 µg of each GFP variant was analyzed by electrophoresis in a 10% denaturing polyacrylamide gel and stained with Coomassie brilliant blue dye. 0.2 µg of the same protein samples in 25 mM Tris pH 8.0 with 100 mM NaCl was placed in a 0.2 mL Eppendorf tube and photographed under UV light (360 nm).

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Thermal Denaturation and Aggregation (FIG. 3a).

Purified GFP variants were diluted to 2 mg/mL in 25 mM Tris pH 8.0, 100 mM NaCl, and 10 mM beta-mercaptoethanol (BME), then photographed under UV illumination ("native"). The samples were heated to 100° C. for 1 minute, then photographed again under UV illumination ("boiled"). Finally, the samples were cooled 2 h at room temperature and photographed again under UV illumination ("cooled").

Chemically Induced Aggregation (FIG. 3b).

2,2,2-trifluoroethanol (TFE) was added to produce solutions with 1.5 mg/mL protein, 25 mM Tris pH 7.0, 10 mM BME, and 40% TFE. Aggregation at 25° C. was monitored by right-angle light scattering.

Size-Exclusion Chromatography (Table 1).

The multimeric state of SAV and GST variants was determined by analyzing 20-50 µg of protein on a Superdex 75 gel-filtration column. Buffer was 100 mM NaCl, 50 mM potassium phosphate pH 7.5. Molecular weights were determined by comparison with a set of monomeric protein standards of known molecular weights analyzed separately under identical conditions.

TABLE 1

Calculated and experimentally determined protein properties.											
name	MW (kD)	length (aa)	$n_{pos}$	$n_{neg}$	$n_{charged}$	$Q_{net}$	pI	$\Delta G$ (kcal/mol) <sup>a</sup>	native MW (kD) <sup>b</sup>	% soluble after boiling <sup>c</sup>	
GFP (-30)	27.8	248	19	49	68	-30	4.8	10.2	n.d.	98	
GFP (-25)	27.8	248	21	46	67	-25	5.0	n.d.	n.d.	n.d.	
sfGFP	27.8	248	27	34	61	-7	6.6	11.2	n.d.	4	
GFP (+36)	28.5	248	56	20	76	+36	10.4	8.8	n.d.	97	
GFP (+48)	28.6	248	63	15	78	+48	10.8	7.1	n.d.	n.d.	
SAV (-40)	14.3	137	5	15	20	-10	5.1	n.d.	55 ± 5 (tetramer)	99	
wtSAV	13.3	128	8	9	17	-1	6.5	n.d.	50 ± 5 (tetramer)	7	
SAV (+52)	14.5	137	16	3	19	+13	10.3	n.d.	55 ± 5 (tetramer)	97	
GST (-40)	24.7	217	17	37	54	-20	4.8	n.d.	50 ± 5 (dimer)	96	
wtGST	24.6	217	24	23	47	+1	7.9	n.d.	50 ± 5 (dimer)	3	
GST (+50) <sup>d</sup>	24.7	217	39	14	53	+25	10.0	n.d.	n.d.	n.d.	

$n_{pos}$ : number of positively charged amino acids (per monomer)

$n_{neg}$ : number of negatively charged amino acids

$n_{charged}$ : total number of charged amino acids

$Q_{net}$ : theoretical net charge at neutral pH

pI, calculated isoelectric point

n.d., not determined

<sup>a</sup>measured by guanidinium denaturation (FIG. 2c).

<sup>b</sup>measured by size-exclusion chromatography.

<sup>c</sup>percent protein remaining in supernatant after 5 min at 100° C., cooling to 25° C., and brief centrifugation.

<sup>d</sup>protein failed to express in *E. coli*.

## OTHER EMBODIMENTS

Those of ordinary skill in the art will readily appreciate that the foregoing represents merely certain preferred embodiments of the invention. Various changes and modifications to the procedures and compositions described above can be made without departing from the spirit or scope of the present invention, as set forth in the following claims.

## APPENDIX A

```
#!/usr/local/bin/perl
#####
#
# avnapsa
#
# prints list of AvNAPSA values for the specified PDB
#
# Mike Lawrence/Kevin Phillips 3/17/2006
#
#####
```

## APPENDIX A-continued

```

sub show_usage
{
    print "\n",
    "Usage: avnapsa <start_pdb> [params]\n",
    "  -3  use 3-letter aa abbreviations (default)\n",
    "  -1  use 1-letter aa abbreviations\n",
    "  -onecol  print one column only (i.e. only the AvNAPSA results)\n\n";
}
##### global variables #####
@atoms;
# fields loaded from PDB:
# type
# atomNum
# atomName
# resName
# chain
# resNum
# x, y, z
# computed fields
# neighborCount
@distances;
@residues;
# fields copied from PDB
# resNum (PDB numbering)
# resName
# computed fields
# avNapsa
#####
## parse command line
$use3or1 = 3;
$onecol_flag = 0;
$start_pdb = $ARGV[0];
for (my $a = 1; $a < @ARGV; ++$a)
{
    if ($ARGV[$a] eq "-1") { $use3or1 = 1; }
    elsif ($ARGV[$a] eq "-3") { $use3or1 = 3; }
    elsif ($ARGV[$a] eq "-onecol") { $onecol_flag = 1; }
    else { show_usage( ); die "Invalid argument $ARGV[$a]\n"; }
}
unless (lc $start_pdb =~ /\.pdb/) { show_usage( ); die "No starting pdb
specified.\n"; }
## read PDB and compute molecular parameters
read_PDB($start_pdb);
tabulate_residues( );
$res = @residues;
compute_distances( );
compute_neighbor_counts( );
compute_residue_avNapsa( );
print_residues( );
exit;
#
# print_residues
#
#
sub print_residues
{
    for (my $r = 0; $r < @residues; $r++)
    {
        my $name = $residues[$r]{resName};
        $name = toggle31($name) if ($use3or1 == 1);
        printf "%d %s AvNAPSA ", $residues[$r]{resNum}, $name unless
$onecol_flag;
        printf "%.0f\n", $residues[$r]{avNapsa};
    }
    print "\nNum residues = ", $#residues+1, "\n\n" unless $onecol_flag;
}
#
# tabulate_residues
#
# goes through list of atoms and makes a list of amino acid residues
# and stores it in global variable @residues
#
sub tabulate_residues
{
    for ($a = 0; $a < @atoms; $a++)
    {
        $resNum = $atoms[$a]{resNum};
        if ( ! resNum_exists($resNum) )
        {
            push @residues,

```

## APPENDIX A-continued

---

```

        {
            resNum => $resNum,
            resName => $atoms[$a]{resName}
        };
    }
}
#
# resNum_exists
#
# returns 1 if resNum is contained in @residues
#
sub resNum_exists($)
{
    my ($resNum) = @_;
    for ($r = 0; $r < @residues; $r++)
    {
        return 1 if ($residues[$r]{resNum} == $resNum);
    }
    return 0;
}
#
# resNum_to_resindex
#
# converts PDB numbering to index in @residues
#
sub resNum_to_resindex($)
{
    my ($resNum) = @_;
    for ($r = 0; $r < @residues; $r++)
    {
        return $r if ($residues[$r]{resNum} == $resNum);
    }
    return "none";
}
#
# readPDB(filename)
#
# reads the atoms from a PDB and returns them as an array of hashes
#
sub read_PDB($)
{
    my ($filename) = @_;
    open (PDB, $filename) or die("Could not open $filename\n");
    $#atoms = -1;      # clear atoms storage
    # read the file
    foreach (<PDB>) {
        my $type = trim(substr($_, 0, 6));      # RType field is columns 1-6
        next unless ($type eq "ATOM" || $type eq "HETATM");
        my $resName = trim(substr($_, 17, 3));  # Res field is columns 18-
20      my $atomName = trim(substr($_, 12, 4));  # Atm field is columns
13-16   next if uc $resName eq "HOH";           # omit waters
        next if uc $atomName =~ /\[0-9\]*H/;    # omit protons
        # add a hash to the array, containing data from this record of the PDB
        push @atoms, {
            type =>      $type,
            resName =>   $resName,
            atomName =>  $atomName,
            atomNum =>   trim(substr($_, 6, 5)),  # Num field is columns 7-11
            chain =>     trim(substr($_, 21, 1)), # Chain field is column 22
            resNum =>     trim(substr($_, 22, 4)), # ResNo field is columns 23-26
            x =>          trim(substr($_, 30, 8)), # X field is columns 31-38
            y =>          trim(substr($_, 38, 8)), # Y field is columns 39-46
            z =>          trim(substr($_, 46, 8)), # Z field is columns 37-54
        };
    }
    close(PDB);
}
#
# trim
#
# removes whitespace from start and end of string
#
sub trim($)
{
    my ($string) = @_;      # retrieve the passed argument
    $string =~ s/\s+//;     # remove leading whitespace
    $string =~ s/\s+$//;    # remove trailing whitespace
}

```

## APPENDIX A-continued

---

```

    return $string;
}
#
# is_number
#
# returns 1 if passed argument is a number (allows whitespace, negative, and
# decimal point)
# returns 0 if passed argument is blank or not a number
#
A
sub is_number($)
{
    $_ = shift;
    s/^s+//;
    s/^s+$/;
    return 1 if /^-[0-9]+$/ || /^-[0-9]*\.[0-9]+$/ || /^-[0-9]+\.[0-9]*$/;
    return 0;
}
#
# inter_residue_distance
#
# returns the minimum distance between any atoms of the specified residues
# (residues are specified according to index in @residues)
#
sub inter_residue_distance($, $)
{
    my ($r1, $r2) = @_;
    ## convert to PDB numbering
    my $resNum1 = $residues[$r1]{resNum};
    my $resNum2 = $residues[$r2]{resNum};
    my $min_dist = 1000000;
    for ($a1 = 0; $a1 < @atoms; ++$a1)
    {
        next unless ( $atoms[$a1]{resNum} == $resNum1 );
        for ($a2 = 0; $a2 < @atoms; ++$a2)
        {
            next unless ( $atoms[$a2]{resNum} == $resNum2 );
            my $dist = $distances[$a1][$a2];
            $min_dist = $dist if ($dist < $min_dist);
        }
    }
    return $min_dist;
}
#
# compute_distances
#
# computes the distances between all atoms
#
sub compute_distances
{
    for(my $atom1=0; $atom1 < @atoms; $atom1++)
    {
        for(my $atom2=$atom1; $atom2 < @atoms; $atom2++)
        {
            my ($x1,$y1,$z1) = ($atoms[$atom1]->{x}, $atoms[$atom1]->{y},
$atoms[$atom1]->{z});
            my ($x2,$y2,$z2) = ($atoms[$atom2]->{x}, $atoms[$atom2]->{y},
$atoms[$atom2]->{z});
            my $distance = sqrt(($x1-$x2)**2 + ($y1-$y2)**2 + ($z1-$z2)**2);
            $distances[$atom1][$atom2] = $distance;
            $distances[$atom2][$atom1] = $distance;
        }
    }
}
#
# compute_neighbor_counts
#
# computes the number of neighbors that each atom has.
# paramter is the cutoff, in Angstroms, for atomic neighborhood
#
sub compute_neighbor_counts
{
    $DISTANCE_CUTOFF = 10;      # criterion for neighborhood, in Angstroms
    for ($atom1=0; $atom1 < @atoms; $atom1++)
    {
        my $count = 0;
        for ($atom2=0; $atom2 < @atoms; $atom2++)
        {
            $count++ if ($distances[$atom1][$atom2] <= $DISTANCE_CUTOFF
&& $atom1 != $atom2);
        }
    }
}

```

## APPENDIX A-continued

---

```

    }
    $atoms[$atom1]{neighborCount} = $count;
  }
}
#
# compute_residue_avNapsa
#
# for each residue, compute
# Average Neighbor Atoms Per Sidechain Atom (AvNAPSA)
# (sidechain atoms are all those except N, C, O, CA)
# for glycines, just use CA
#
sub compute_residue_avNapsa
{
  for (my $r = 0; $r < @residues; $r++)
  {
    my $numSideChainAtoms = 0;
    my $totalNeighbors = 0;
    my $resName = $residues[$r]{resName};
    my $resNum = $residues[$r]{resNum};
A
    for (my $a = 0; $a < @atoms; $a++)
    {
      if ($atoms[$a]{resNum} == $resNum)
      {
        my $atomName = $atoms[$a]{atomName};
        if (
          (
            $atomName ne "C"
            && $atomName ne "O"
            && $atomName ne "N"
            && $atomName ne "CA"
          )
          || ( $atomName eq "CA" && $resName eq "GLY")
        )
        {
          $numSideChainAtoms++;
          $totalNeighbors += $atoms[$a]{neighborCount};
        }
      }
    }
    my $avNapsa = $totalNeighbors / $numSideChainAtoms;
    $residues[$r]{avNapsa} = $avNapsa;
  }
}
#
# toggle31
#
# converts 3-letter abbrev to 1-letter
# or 1-letter abbrev to 3-letter
#
sub toggle31($)
{
  %conv3to1 = ( "ALA" => "A", "CYS" => "C", "SER" => "S", "LEU" => "L",
    "ILE" => "I", "PHE" => "F", "ARG" => "R", "ASN" => "N", "GLN" => "Q",
    "TYR" => "Y", "LYS" => "K", "ASP" => "D", "GLU" => "E", "VAL" => "V",
    "TRP" => "W", "MET" => "M", "HIS" => "H", "GLY" => "G", "PRO" => "P",
    "THR" => "T" );
  %conv1to3 = reverse %conv3to1;
  my ($abbrev) = @_;
  $abbrev = uc $abbrev;
  return $conv1to3{$abbrev} if length ($abbrev) == 1;
  return $conv3to1{$abbrev} if length ($abbrev) == 3;
  die "in toggle31( ): invalid amino acid abbreviation $abbrev\n";
}
#
# is_aa
#
# returns 1 if passed argument is a 1-letter amino acid
#
sub is_aa($)
{
  my ($string) = @_;
  return 1 if (length toggle31($string) == 3);
  return 0;
}

```

---

## SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 37

<210> SEQ ID NO 1

<211> LENGTH: 238

<212> TYPE: PRT

<213> ORGANISM: *Aequorea victoria*

<400> SEQUENCE: 1

```

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1          5          10          15
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20        25        30
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35        40        45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50        55        60
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65        70        75        80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85        90        95
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100       105       110
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115       120       125
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130       135       140
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145       150       155       160
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165       170       175
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180       185       190
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195       200       205
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210       215       220
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225       230       235

```

<210> SEQ ID NO 2

<211> LENGTH: 248

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Surface modified green fluorescent protein  
(GFP) from *Aequorea victoria*

<400> SEQUENCE: 2

```

Met Gly His His His His His His Gly Gly Ala Ser Lys Gly Glu Glu
1          5          10          15
Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val
20        25        30
Asn Gly His Glu Phe Ser Val Arg Gly Glu Gly Glu Gly Asp Ala Thr
35        40        45
Glu Gly Glu Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Glu Leu Pro
50        55        60
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys

```

-continued

---

65	70	75	80
Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser	85	90	95
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Ser Phe Lys Asp	100	105	110
Asp Gly Thr Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	115	120	125
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	130	135	140
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asp Val	145	150	155
Tyr Ile Thr Ala Asp Lys Gln Glu Asn Gly Ile Lys Ala Glu Phe Glu	165	170	175
Ile Arg His Asn Val Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	180	185	190
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asp	195	200	205
His Tyr Leu Ser Thr Glu Ser Ala Leu Ser Lys Asp Pro Asn Glu Asp	210	215	220
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Asp	225	230	235
His Gly Met Asp Glu Leu Tyr Lys	245		

<210> SEQ ID NO 3  
 <211> LENGTH: 248  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Surface modified green fluorescent protein  
 (GFP) from *Aequorea victoria*

<400> SEQUENCE: 3

Met Gly His His His His His His Gly Gly Ala Ser Lys Gly Glu Glu	1	5	10	15
Leu Phe Asp Gly Glu Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val	20	25	30	
Asn Gly His Glu Phe Ser Val Arg Gly Glu Gly Glu Gly Asp Ala Thr	35	40	45	
Glu Gly Glu Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Glu Leu Pro	50	55	60	
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys	65	70	75	80
Phe Ser Arg Tyr Pro Asp His Met Asp Gln His Asp Phe Phe Lys Ser	85	90	95	
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Ser Phe Lys Asp	100	105	110	
Asp Gly Thr Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	115	120	125	
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	130	135	140	
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asp Val	145	150	155	160
Tyr Ile Thr Ala Asp Lys Gln Glu Asn Gly Ile Lys Ala Glu Phe Glu	165	170	175	



-continued

---

```

Ile Arg His Asn Val Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
      180                      185                      190

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asp
      195                      200                      205

His Tyr Leu Ser Thr Glu Ser Ala Leu Ser Lys Asp Pro Asn Glu Asp
      210                      215                      220

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Asp
      225                      230                      235                      240

His Gly Met Asp Glu Leu Tyr Lys
      245

<210> SEQ ID NO 4
<211> LENGTH: 248
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Surface modified green fluorescent protein
                        (GFP) from Aequorea victoria

<400> SEQUENCE: 4

Met Gly His His His His His His Gly Gly Ala Ser Lys Gly Glu Glu
 1          5          10          15

Leu Phe Asp Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val
 20          25          30

Asn Gly His Glu Phe Ser Val Arg Gly Glu Gly Glu Gly Asp Ala Thr
 35          40          45

Glu Gly Glu Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Glu Leu Pro
 50          55          60

Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys
 65          70          75          80

Phe Ser Asp Tyr Pro Asp His Met Asp Gln His Asp Phe Phe Lys Ser
 85          90          95

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Ser Phe Lys Asp
100          105          110

Asp Gly Thr Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
115          120          125

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
130          135          140

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asp Val
145          150          155          160

Tyr Ile Thr Ala Asp Lys Gln Glu Asn Gly Ile Lys Ala Glu Phe Glu
165          170          175

Ile Arg His Asn Val Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
      180                      185                      190

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asp
      195                      200                      205

His Tyr Leu Ser Thr Glu Ser Ala Leu Ser Lys Asp Pro Asn Glu Asp
      210                      215                      220

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Asp
      225                      230                      235                      240

His Gly Met Asp Glu Leu Tyr Lys
      245

```

```

<210> SEQ ID NO 5
<211> LENGTH: 248
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

```

-continued

<220> FEATURE:  
 <223> OTHER INFORMATION: Surface modified green fluorescent protein  
 (GFP) from *Aequorea victoria*

<400> SEQUENCE: 5

```

Met Gly His His His His His His Gly Gly Ala Ser Lys Gly Glu Arg
1           5           10           15

Leu Phe Arg Gly Lys Val Pro Ile Leu Val Glu Leu Lys Gly Asp Val
          20           25           30

Asn Gly His Lys Phe Ser Val Arg Gly Lys Gly Lys Gly Asp Ala Thr
          35           40           45

Arg Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
          50           55           60

Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys
65           70           75           80

Phe Ser Arg Tyr Pro Lys His Met Lys Arg His Asp Phe Phe Lys Ser
          85           90           95

Ala Met Pro Lys Gly Tyr Val Gln Glu Arg Thr Ile Ser Phe Lys Lys
          100          105          110

Asp Gly Lys Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Arg Thr
          115          120          125

Leu Val Asn Arg Ile Lys Leu Lys Gly Arg Asp Phe Lys Glu Lys Gly
130          135          140

Asn Ile Leu Gly His Lys Leu Arg Tyr Asn Phe Asn Ser His Lys Val
145          150          155          160

Tyr Ile Thr Ala Asp Lys Arg Lys Asn Gly Ile Lys Ala Lys Phe Lys
          165          170          175

Ile Arg His Asn Val Lys Asp Gly Ser Val Gln Leu Ala Asp His Tyr
          180          185          190

Gln Gln Asn Thr Pro Ile Gly Arg Gly Pro Val Leu Leu Pro Arg Asn
          195          200          205

His Tyr Leu Ser Thr Arg Ser Lys Leu Ser Lys Asp Pro Lys Glu Lys
210          215          220

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Lys
225          230          235          240

His Gly Arg Asp Glu Arg Tyr Lys
          245
  
```

<210> SEQ ID NO 6  
 <211> LENGTH: 248  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Surface modified green fluorescent protein  
 (GFP) from *Aequorea victoria*

<400> SEQUENCE: 6

```

Met Gly His His His His His His Gly Gly Arg Ser Lys Gly Lys Arg
1           5           10           15

Leu Phe Arg Gly Lys Val Pro Ile Leu Val Glu Leu Lys Gly Asp Val
          20           25           30

Asn Gly His Lys Phe Ser Val Arg Gly Lys Gly Lys Gly Asp Ala Thr
          35           40           45

Arg Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
          50           55           60

Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys
65           70           75           80
  
```



-continued

180	185	190	
Gln Gln Asn Thr Pro Ile Gly Arg Gly Pro Val Leu Leu Pro Arg Lys			
195	200	205	
His Tyr Leu Ser Thr Arg Ser Lys Leu Ser Lys Asp Pro Lys Glu Lys			
210	215	220	
Arg Asp His Met Val Leu Lys Glu Phe Val Thr Ala Ala Gly Ile Lys			
225	230	235	240
His Gly Arg Lys Glu Arg Tyr Lys			
245			
<210> SEQ ID NO 8			
<211> LENGTH: 747			
<212> TYPE: DNA			
<213> ORGANISM: Artificial Sequence			
<220> FEATURE:			
<223> OTHER INFORMATION: Surface modified green fluorescent protein (GFP) from <i>Aequorea victoria</i>			
<400> SEQUENCE: 8			
atggggcatc accatcatca tcatggcggg gcgtctaagg gggaggagtt atttacgggt	60		
gtggtgccga tcctggtgga gcttgatggc gatgttaacg gccatgaatt ttctgtccgc	120		
ggtgaagggg aggggtgatgc cacggaaggg gagctgacac ttaaatttat ttgcaccacc	180		
ggtgaactcc cgggtcccggtg gccgaccctg gtgaccaccc tgacctacgg cggttcaatgc	240		
ttttcacgtt atccggatca catgaagcaa cacgacttct taaaagcgc gatgcctgaa	300		
ggctatgttc aagaacgtac aattagtttt aaagatgacg gcacctacaa gaccctgctg	360		
gaagtaaaat ttgaagggga cacttttagtg aaccgcatcg agctgaaagg gatcgatttt	420		
aaagaagatg ggaatatact gggacacaaa cttgaataca actttaatag tcatgacgtc	480		
tatatcacgg cggacaaaaca ggaaaacgga attaaggcag aatttgagat tcggcataat	540		
gtcgaagatg gctcgggtaca gttggctgat cactatcagc agaatacggc gattggagat	600		
ggtccggttt tattaccaga cgatcactat ctgtccaccg aatccgccct gagcaaagat	660		
ccgaatgaag accgggacca tatggttctg ctggaatttg ttacggcggc tggatttgac	720		
catggcatgg atgagctgta taagtag	747		
<210> SEQ ID NO 9			
<211> LENGTH: 747			
<212> TYPE: DNA			
<213> ORGANISM: Artificial Sequence			
<220> FEATURE:			
<223> OTHER INFORMATION: Surface modified green fluorescent protein (GFP) from <i>Aequorea victoria</i>			
<400> SEQUENCE: 9			
atggggcatc accatcatca tcatggcggg gcgtctaagg gggaggagtt atttgatggt	60		
gaagtgccga tcctggtgga gcttgatggc gatgttaacg gccatgaatt ttctgtccgc	120		
ggtgaagggg aggggtgatgc cacggaaggg gagctgacac ttaaatttat ttgcaccacc	180		
ggtgaactcc cgggtcccggtg gccgaccctg gtgaccaccc tgacctacgg cggttcaatgc	240		
ttttcacgtt atccggatca catggaccaa cacgacttct taaaagcgc gatgcctgaa	300		
ggctatgttc aagaacgtac aattagtttt aaagatgacg gcacctacaa gaccctgctg	360		
gaagtaaaat ttgaagggga cacttttagtg aaccgcatcg agctgaaagg gatcgatttt	420		
aaagaagatg ggaatatact gggacacaaa cttgaataca actttaatag tcatgacgtc	480		
tatatcacgg cggacaaaaca ggaaaacgga attaaggcag aatttgagat tcggcataat	540		

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```

gtcgaagatg gctcgggtaca gttggctgat cactatcagc agaatacgcc gattggagat 600
gggtccggttt tattaccaga cgatcactat ctgtccaccg aatccgccct gagcaaagat 660
ccgaatgaag accgggacca tatggttctg ctggaatttg ttacggcggc tggatttgac 720
catggcatgg atgagctgta taagtag 747

```

```

<210> SEQ ID NO 10
<211> LENGTH: 747
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Surface modified green fluorescent protein
(GFP) from Aequorea victoria

```

```

<400> SEQUENCE: 10

```

```

atggggcatc accatcatca tcatggcggg gcgtctaagg gggaggagtt atttgatggt 60
gtggtgccga tcctgggtgga gcttgatggc gatgttaacg gccatgaatt ttctgtccgc 120
ggatgaagggg aggggtgatgc cacggaaggg gagctgacac ttaaatttat ttgcaccacc 180
ggatgaactcc cgggtcccggtg gccgaccctg gtgaccaccc tgacctacgg cgttcaatgc 240
ttttcagatt atccggatca catggaccaa cagcacttct taaaagcgc gatgcctgaa 300
ggctatgttc aagaacgtac aattagtttt aaagatgacg gcacctacaa gacctgtgcg 360
gaagtaaaat ttgaagggga cacttttagtg aaccgcacgc agctgaaagg gatcgatttt 420
aaagaagatg ggaatatcct gggacacaaa ctgtaataca actttaatag tcatgacgtc 480
tatatcacgg cggacaaaaca ggaaaacgga attaaggcag aatttgagat tcggcataat 540
gtcgaagatg gctcgggtaca gttggctgat cactatcagc agaatacgcc gattggagat 600
gggtccggttt tattaccaga cgatcactat ctgtccaccg aatccgccct gagcaaagat 660
ccgaatgaag accgggacca tatggttctg ctggaatttg ttacggcggc tggatttgac 720
catggcatgg atgagctgta taagtag 747

```

```

<210> SEQ ID NO 11
<211> LENGTH: 747
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Surface modified green fluorescent protein
(GFP) from Aequorea victoria

```

```

<400> SEQUENCE: 11

```

```

atggggcatc atcatcatca ccacggcggg gcgtctaagg gagagcgctt gtttcgcggc 60
aaagtcccca ttcttgtgga gtcacaaggt gatgtaaatg gtcataaatt tagtgtgcgc 120
gggaaaggga aaggagatgc tacgcggggc aagctcaccg tgaaatttat ttgcacaacc 180
ggcaaaactgc cagtgcctgtg gcctacatta gtcactactc tgacgtacgg tgttcagtgc 240
ttttctcgct atcccaaaaca catgaaacgc catgatttct tcaagagcgc gatgccaaaa 300
ggttatgtgc aggaacgcac catcagcttt aaaaaagacg gcaaatataa aacctgtgca 360
gaagttaaat tcgaaggccg caccctggtc aaccgcatta aactgaaagg tcgtgacttc 420
aaagagaaa gtaatatctt tggtcacaaa ctgcgtata attcaactc tcacaaagt 480
tatattacgg cggataaacg taaaaacggg attaaagcga aatttaagat tcgtcataat 540
gttaaagacg gcagtgtgca gtttagcgat cattatcagc agaatacccc aattgggtgc 600
gggtccagtgc tgctgccgcg taaccattat ctgtcgaccc gcagcaaaact cagcaaagac 660

```

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```
ccgaaagaaa aacgtgacca catggtatta ctggaatttg tgaccgcagc aggcattaaa 720
catggccgcg atgaacgtta caaatag 747
```

```
<210> SEQ ID NO 12
<211> LENGTH: 747
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Surface modified green fluorescent protein
(GFP) from Aequorea victoria
```

```
<400> SEQUENCE: 12
```

```
atgggccatc atcatcacca ccacggcggc cgctcaaaag gtaaacgctt gttccgtggt 60
aaagtaccga tcttagtgga gctcaaagg gatgtgaatg gccataagtt ctcggttcgt 120
ggcaaaggtg agggagatgc gacgcgcggc aaattaacgc tgaaattcat ttgtactaca 180
ggtaaaactgc cgggtgccatg gcctactctc gtcaccacgt tgacctatgg ggttcaatgc 240
ttcagccggt accctaaaca catgaagcgc cagcatttct tcaaatcggc gatgccaaag 300
gggtatgtcc aggaacgcac tatcagcttc aaaaagacg gtaagtataa aactcgtgct 360
gaagttaaat tcgaaggacg cactcgtgta aatcgcatta aattgaagg ggcgcacttt 420
aaggaaaaag gtaatatctt aggtcacaaa ttgcgtaca acttcaactc tcataaagtt 480
tacattacag cagataagcg taaaaatggc atcaaagcga aattcaaaat tcgtcacaat 540
gtgaaagatg gtagcgtgca attagccgat cattaccagc agaatacgcc gatcggtcgc 600
ggcccagtac tgttgccgcg caaacattac ttatctaccc ggagtaaact gtctaagac 660
ccaaaagaga agcgcgacca tatggttctc ctggagtttg tcaccgcgcg cggaattaaa 720
cacggccgca aagagcgcta taaatag 747
```

```
<210> SEQ ID NO 13
<211> LENGTH: 747
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Surface modified green fluorescent protein
(GFP) from Aequorea victoria
```

```
<400> SEQUENCE: 13
```

```
atgggccacc atcatcatca ccacggggga cgctctaaag gtaaacgtct gtttcgtgga 60
aagggtccca ttctggttaa actcaaagg gatgtcaacg gccataagtt ttcggttcgt 120
ggcaaaggtg aagggtgatgc gacgcgcggg aaattaacac tgaaatttat ttgcacaacc 180
ggaaaactcc ctgtgcgctg gccgactttg gtgaccacat taacctatgg tgttcaatgc 240
ttctcacgtt atccgaagca tatgaaacgt catgattttt tcaaatcggc tatgccgaaa 300
ggttacgtcc aggagcgcac catctcattt aagaaagacg gtaagtataa aaccctgtgct 360
gaagtataat tcaaaggacg caccctggtg aatcgcatta aactgaaagg tcgtgatttc 420
aaagaaaagg gaaatatctt agggcataag ctccgttata attttaacag tcataagggtg 480
tatattaccg ctgataaacg caaaaacgga atcaaagcga aatttaagat ccgtcataat 540
gtaaaagatg gctcagtcca actggcaaaa cattaccagc agaatacccc gatcggccgc 600
ggtcctgtgc ttctgcgcg taaacactac ttgtcgaccc ggtcaaaatt gagtaagat 660
ccgaagggaa agcgtgatca catggtcttg aaggaatttg taactgcagc aggtattaaa 720
cacgggcgca aagaacgtta caaatag 747
```

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<210> SEQ ID NO 14
<211> LENGTH: 128
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Wild type streptavidin

<400> SEQUENCE: 14
Ala Ala Glu Ala Gly Ile Thr Gly Thr Trp Tyr Asn Gln Leu Gly Ser
1          5          10          15
Thr Phe Ile Val Thr Ala Gly Ala Asp Gly Ala Leu Thr Gly Thr Tyr
20          25          30
Glu Ser Ala Val Gly Asn Ala Glu Ser Arg Tyr Val Leu Thr Gly Arg
35          40          45
Tyr Asp Ser Ala Pro Ala Thr Asp Gly Ser Gly Thr Ala Leu Gly Trp
50          55          60
Thr Val Ala Trp Lys Asn Asn Tyr Arg Asn Ala His Ser Ala Thr Thr
65          70          75          80
Trp Ser Gly Gln Tyr Val Gly Gly Ala Glu Ala Arg Ile Asn Thr Gln
85          90          95
Trp Leu Leu Thr Ser Gly Thr Thr Glu Ala Asn Ala Trp Lys Ser Thr
100         105         110
Leu Val Gly His Asp Thr Phe Thr Lys Val Lys Pro Ser Ala Ala Ser
115         120         125

<210> SEQ ID NO 15
<211> LENGTH: 137
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Surface modified streptavidin (SAV-NEG40)

<400> SEQUENCE: 15
Met Gly His His His His His His Gly Gly Ala Glu Ala Gly Ile Thr
1          5          10          15
Gly Thr Trp Tyr Asn Gln Leu Gly Ser Thr Phe Ile Val Thr Ala Gly
20          25          30
Ala Asp Gly Ala Leu Thr Gly Thr Tyr Glu Ser Ala Val Gly Asp Ala
35          40          45
Glu Ser Glu Tyr Val Leu Thr Gly Arg Tyr Asp Ser Ala Pro Ala Thr
50          55          60
Asp Gly Ser Gly Thr Ala Leu Gly Trp Thr Val Ala Trp Lys Asn Asp
65          70          75          80
Tyr Glu Asn Ala His Ser Ala Thr Thr Trp Ser Gly Gln Tyr Val Gly
85          90          95
Gly Ala Glu Ala Arg Ile Asn Thr Gln Trp Leu Leu Thr Ser Gly Thr
100         105         110
Thr Glu Ala Asp Ala Trp Lys Ser Thr Leu Val Gly His Asp Thr Phe
115         120         125
Thr Lys Val Glu Pro Ser Ala Ala Ser
130         135

<210> SEQ ID NO 16
<211> LENGTH: 137
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Surface modified streptavidin (SAV-POS52)

<400> SEQUENCE: 16

```

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Met Gly His His His His His His Gly Gly Ala Lys Ala Gly Ile Thr  
 1 5 10 15  
 Gly Thr Trp Tyr Asn Gln Leu Gly Ser Thr Phe Ile Val Thr Ala Gly  
 20 25 30  
 Ala Lys Gly Ala Leu Thr Gly Thr Tyr Glu Ser Ala Val Gly Asn Ala  
 35 40 45  
 Lys Ser Arg Tyr Val Leu Thr Gly Arg Tyr Asp Ser Ala Pro Ala Thr  
 50 55 60  
 Lys Gly Ser Gly Thr Ala Leu Gly Trp Thr Val Ala Trp Lys Asn Lys  
 65 70 75 80  
 Tyr Arg Asn Ala His Ser Ala Thr Thr Trp Ser Gly Gln Tyr Val Gly  
 85 90 95  
 Gly Ala Lys Ala Arg Ile Asn Thr Gln Trp Leu Leu Thr Ser Gly Thr  
 100 105 110  
 Thr Lys Ala Lys Ala Trp Lys Ser Thr Leu Val Gly His Asp Thr Phe  
 115 120 125  
 Thr Lys Val Lys Pro Ser Ala Ala Ser  
 130 135

<210> SEQ ID NO 17  
 <211> LENGTH: 442  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Surface modified streptavidin (SAV-NEG40)

<400> SEQUENCE: 17

```

ggttcagcca tgggtcatca ccaccacat cacggtggcg ccgaagcagg tattaccggt      60
acctgggtata accagttagg ctcaaccttt attgtgaccg cgggagcgga cggcgccctta    120
accggtacct acgaatcagc tgtaggtgac gcggaatcag agtacgtatt aaccggtcgt      180
tatgatagcg cgccggcgac tgacggtagc ggtactgctt taggttggac cgtagcgtgg      240
aagaatgatt atgaaaacgc acatagcgca acaacgtggt cagggcagta cgttggcgga      300
gctgaggcgc gcattaacac gcagtgggta ttaactagcg gcaccactga agctgatgcc      360
tggaagagca cgtttagtggg tcattgatacc ttcactaaag tggaaccttc agctgcgtca    420
taataatgac tcgagacctg ca                                         442

```

<210> SEQ ID NO 18  
 <211> LENGTH: 442  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Surface modified streptavidin (SAV-POS52)

<400> SEQUENCE: 18

```

ggttcagcca tgggtcatca ccaccacat cacggtggcg ccaaagcagg tattaccggt      60
acctgggtata accagttagg ctcaaccttt attgtgaccg cgggagcgaa aggcgccctta    120
accggtacct acgaatcagc tgtaggaaac gcaaaatcac gctacgtatt aaccggtcgt      180
tatgatagcg cgccggcgac taaaggtagc ggtactgctt taggttggac cgtagcgtgg      240
aagaataagt atcgtaatgc gcacagtgc accacttggt cagggcagta cgtaggggga      300
gccaaagcac gtatcaacac gcagtgggta ttaacatcag gtaccaccaa agcgaaagcc      360
tggaagagca cgtttagtggg tcattgatacc ttcactaaag tgaaaccttc agctgcgtca    420
taataatgac tcgagacctg ca                                         442

```



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<210> SEQ ID NO 19  
 <211> LENGTH: 217  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Wild Type glutathione-S-transferase (GST)

<400> SEQUENCE: 19

```

Met Gly His His His His His His Gly Gly Pro Pro Tyr Thr Ile Thr
1          5          10          15
Tyr Phe Pro Val Arg Gly Arg Cys Glu Ala Met Arg Met Leu Leu Ala
20          25          30
Asp Gln Asp Gln Ser Trp Lys Glu Glu Val Val Thr Met Glu Thr Trp
35          40          45
Pro Pro Leu Lys Pro Ser Cys Leu Phe Arg Gln Leu Pro Lys Phe Gln
50          55          60
Asp Gly Asp Leu Thr Leu Tyr Gln Ser Asn Ala Ile Leu Arg His Leu
65          70          75          80
Gly Arg Ser Phe Gly Leu Tyr Gly Lys Asp Gln Lys Glu Ala Ala Leu
85          90          95
Val Asp Met Val Asn Asp Gly Val Glu Asp Leu Arg Cys Lys Tyr Ala
100         105         110
Thr Leu Ile Tyr Thr Asn Tyr Glu Ala Gly Lys Glu Lys Tyr Val Lys
115         120         125
Glu Leu Pro Glu His Leu Lys Pro Phe Glu Thr Leu Leu Ser Gln Asn
130         135         140
Gln Gly Gly Gln Ala Phe Val Val Gly Ser Gln Ile Ser Phe Ala Asp
145         150         155         160
Tyr Asn Leu Leu Asp Leu Leu Arg Ile His Gln Val Leu Asn Pro Ser
165         170         175
Cys Leu Asp Ala Phe Pro Leu Leu Ser Ala Tyr Val Ala Arg Leu Ser
180         185         190
Ala Arg Pro Lys Ile Lys Ala Phe Leu Ala Ser Pro Glu His Val Asn
195         200         205
Arg Pro Ile Asn Gly Asn Gly Lys Gln
210         215

```

<210> SEQ ID NO 20  
 <211> LENGTH: 217  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Surface modified glutathione-S-transferase  
 (GST-NEG40)

<400> SEQUENCE: 20

```

Met Gly His His His His His His Gly Gly Pro Pro Tyr Thr Ile Thr
1          5          10          15
Tyr Phe Pro Val Arg Gly Arg Cys Glu Ala Met Arg Met Leu Leu Ala
20          25          30
Asp Gln Asp Gln Ser Trp Glu Glu Glu Val Val Thr Met Glu Thr Trp
35          40          45
Pro Pro Leu Lys Pro Ser Cys Leu Phe Arg Gln Leu Pro Lys Phe Gln
50          55          60
Asp Gly Asp Leu Thr Leu Tyr Gln Ser Asn Ala Ile Leu Arg His Leu
65          70          75          80

```

Gly	Arg	Ser	Phe	Gly	Leu	Tyr	Gly	Glu	Asp	Glu	Glu	Glu	Ala	Ala	Leu	
			85													
Val	Asp	Met	Val	Asn	Asp	Gly	Val	Glu	Asp	Leu	Arg	Cys	Lys	Tyr	Ala	
			100													
Thr	Leu	Ile	Tyr	Thr	Asp	Tyr	Glu	Ala	Gly	Lys	Glu	Glu	Tyr	Val	Glu	
			115													
Glu	Leu	Pro	Glu	His	Leu	Lys	Pro	Phe	Glu	Thr	Leu	Leu	Ser	Glu	Asn	
			130													
Glu	Gly	Gly	Glu	Ala	Phe	Val	Val	Gly	Ser	Glu	Ile	Ser	Phe	Ala	Asp	
			145													
Tyr	Asn	Leu	Leu	Asp	Leu	Leu	Arg	Ile	His	Gln	Val	Leu	Asn	Pro	Ser	
			165													
Cys	Leu	Asp	Ala	Phe	Pro	Leu	Leu	Ser	Ala	Tyr	Val	Ala	Arg	Leu	Ser	
			180													
Ala	Arg	Pro	Glu	Ile	Glu	Ala	Phe	Leu	Ala	Ser	Pro	Glu	His	Val	Asp	
			195													
Arg	Pro	Ile	Asn	Gly	Asn	Gly	Lys	Gln								
			210													
<210> SEQ ID NO 21																
<211> LENGTH: 217																
<212> TYPE: PRT																
<213> ORGANISM: Artificial Sequence																
<220> FEATURE:																
<223> OTHER INFORMATION: Surface modified glutathione-S-transferase (GST-POS50)																
<400> SEQUENCE: 21																
Met	Gly	His	His	His	His	His	His	Gly	Gly	Pro	Pro	Tyr	Thr	Ile	Thr	
1				5												
Tyr	Phe	Pro	Val	Arg	Gly	Arg	Cys	Glu	Ala	Met	Arg	Met	Leu	Leu	Ala	
			20													
Asp	Gln	Lys	Gln	Ser	Trp	Lys	Glu	Glu	Val	Val	Thr	Met	Lys	Thr	Trp	
			35													
Pro	Pro	Leu	Lys	Pro	Ser	Cys	Leu	Phe	Arg	Gln	Leu	Pro	Lys	Phe	Gln	
			50													
Asp	Gly	Lys	Leu	Thr	Leu	Tyr	Gln	Ser	Asn	Ala	Ile	Leu	Arg	His	Leu	
			65													
Gly	Arg	Ser	Phe	Gly	Leu	Tyr	Gly	Lys	Lys	Gln	Lys	Glu	Ala	Ala	Leu	
			85													
Val	Asp	Met	Val	Asn	Asp	Gly	Val	Glu	Asp	Leu	Arg	Cys	Lys	Tyr	Ala	
			100													
Thr	Leu	Ile	Tyr	Thr	Lys	Tyr	Lys	Ala	Gly	Lys	Lys	Lys	Tyr	Val	Lys	
			115													
Lys	Leu	Pro	Lys	His	Leu	Lys	Pro	Phe	Glu	Thr	Leu	Leu	Ser	Lys	Asn	
			130													
Lys	Gly	Gly	Lys	Ala	Phe	Val	Val	Gly	Ser	Lys	Ile	Ser	Phe	Ala	Asp	
			145													
Tyr	Asn	Leu	Leu	Asp	Leu	Leu	Arg	Ile	His	Gln	Val	Leu	Asn	Pro	Ser	
			165													
Cys	Leu	Lys	Ala	Phe	Pro	Leu	Leu	Ser	Ala	Tyr	Val	Ala	Arg	Leu	Ser	
			180													
Ala	Arg	Pro	Lys	Ile	Lys	Ala	Phe	Leu	Ala	Ser	Pro	Glu	His	Val	Lys	
			195													
Arg	Pro	Ile	Asn	Gly	Asn	Gly	Lys	Gln								
			210													

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<210> SEQ ID NO 22  
 <211> LENGTH: 682  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Surface modified glutathione-S-transferase  
 (GST-NEG40)

<400> SEQUENCE: 22

```

ggttcagcca tgggtcatca ccaccacat cacggtggcc cgccgtacac cattacatac      60
tttccggtac gtggtcggtg tgaagcgatg cgtatgttat tagcggacca ggaccaatca      120
tgggaagaag aagtagtgac aatggaaacc tggcgcgctg taaagcctag ctgtttattc      180
cgtcaattac cgaagtttca ggatggtgat ttaaccttat accagtctaa cgcgatctta      240
cgtcatcttag gtcgctcatt tggttttatac ggtgaagatg aagaagaagc agccttagtg      300
gatatggtga atgatggcgt ggaagactta cgttgtaaat acgcgacggt aatttacact      360
gattatgaag ccggttaaaga ggagtagctg gaagaattac ctgaacacct gaagccggtt      420
gaaacattac tgagcgaaaa tgaaggaggt gaggcggtcg tagttggtag cgaaattagc      480
ttcgctgatt ataacttatt agacttatta cgcattcacc aggtttttaa tcctagctgt      540
ttagacgctt tcccgttact gagcgcatat gtagcgcgcc tgagcgcccg tccggaatt      600
gaagctttct tagcgtcacc tgaacacgta gaccgcccga ttaacggaaa cggaagcag      660
taataatgag gtaccacctg ca                                          682
  
```

<210> SEQ ID NO 23  
 <211> LENGTH: 682  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Surface modified glutathione-S-transferase  
 (GST-POS50)

<400> SEQUENCE: 23

```

ggttcagcca tgggtcatca ccaccacat cacggtggcc cgccgtacac cattacatac      60
tttccggtac gtggtcggtg tgaagcgatg cgtatgttat tagcggacca gaaacaatca      120
tggaaagaag aagtagtgac aatgaagacc tggcgcgctg taaagcctag ctgtttattc      180
cgtcaattac cgaagtttca ggatggtaaa ttaaccttat accagtctaa cgcgatctta      240
cgtcatcttag gtcgctcatt tggttttatac ggtaagaagc agaaagaagc agccttagtg      300
gatatggtga atgatggcgt ggaagactta cgttgtaaat acgcgacggt aatttacact      360
aaatataaag ccggtaaaaa gaagtacgtg aaaaaattac ctaaacacct gaagccggtt      420
gaaacattac tgagcaaaaa taaaggaggt aaggcggtcg tagttggtag caagattagc      480
ttcgctgatt ataacttatt agacttatta cgcattcacc aggtttttaa tcctagctgt      540
ttaaaggctt tcccgttact gagcgcatat gtagcgcgcc tgagcgcccg tccgaagatc      600
aaagctttct tagcgtcacc tgaacacgtg aagcgcccga ttaacggaaa cggaagcag      660
taataatgag gtaccacctg ca                                          682
  
```

<210> SEQ ID NO 24  
 <211> LENGTH: 248  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic Polypeptide

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&lt;400&gt; SEQUENCE: 24

Met Gly His His His His His His Gly Gly Ala Ser Lys Gly Glu Glu  
 1 5 10 15  
 Leu Phe Asp Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val  
 20 25 30  
 Asn Gly His Glu Phe Ser Val Arg Gly Glu Gly Glu Gly Asp Ala Thr  
 35 40 45  
 Glu Gly Glu Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Glu Leu Pro  
 50 55 60  
 Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys  
 65 70 75 80  
 Phe Ser Asp Tyr Pro Asp His Met Asp Gln His Asp Phe Phe Lys Ser  
 85 90 95  
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Ser Phe Lys Asp  
 100 105 110  
 Asp Gly Thr Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 115 120 125  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 130 135 140  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asp Val  
 145 150 155 160  
 Tyr Ile Thr Ala Asp Lys Gln Glu Asn Gly Ile Lys Ala Glu Phe Glu  
 165 170 175  
 Ile Arg His Asn Val Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 180 185 190  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asp  
 195 200 205  
 His Tyr Leu Ser Thr Glu Ser Ala Leu Ser Lys Asp Pro Asn Glu Asp  
 210 215 220  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Asp  
 225 230 235 240  
 His Gly Met Asp Glu Leu Tyr Lys  
 245

&lt;210&gt; SEQ ID NO 25

&lt;211&gt; LENGTH: 248

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic Polypeptide

&lt;400&gt; SEQUENCE: 25

Met Gly His His His His His His Gly Gly Ala Ser Lys Gly Glu Glu  
 1 5 10 15  
 Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val  
 20 25 30  
 Asn Gly His Glu Phe Ser Val Arg Gly Glu Gly Glu Gly Asp Ala Thr  
 35 40 45  
 Glu Gly Glu Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Glu Leu Pro  
 50 55 60  
 Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys  
 65 70 75 80  
 Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser  
 85 90 95  
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Ser Phe Lys Asp

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100					105					110					
Asp	Gly	Thr	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr
	115						120					125			
Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly
	130					135					140				
Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Phe	Asn	Ser	His	Asp	Val
	145					150					155				160
Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Glu	Asn	Gly	Ile	Lys	Ala	Glu	Phe	Glu
				165					170					175	
Ile	Arg	His	Asn	Val	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr
			180					185					190		
Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asp
		195					200					205			
His	Tyr	Leu	Ser	Thr	Glu	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Asp
	210					215					220				
Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Asp
	225					230					235				240
His	Gly	Met	Asp	Glu	Leu	Tyr	Lys								
				245											

&lt;210&gt; SEQ ID NO 26

&lt;211&gt; LENGTH: 248

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic Polypeptide

&lt;400&gt; SEQUENCE: 26

Met	Gly	His	His	His	His	His	Gly	Gly	Ala	Ser	Lys	Gly	Glu	Glu	
1				5				10					15		
Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val
		20					25					30			
Asn	Gly	His	Lys	Phe	Ser	Val	Arg	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr
		35				40						45			
Asn	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro
		50				55					60				
Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys
	65				70				75					80	
Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser
			85					90						95	
Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Ser	Phe	Lys	Asp
		100						105					110		
Asp	Gly	Thr	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr
		115					120					125			
Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly
	130					135					140				
Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Phe	Asn	Ser	His	Asn	Val
	145				150					155					160
Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Ala	Asn	Phe	Lys
			165					170					175		
Ile	Arg	His	Asn	Val	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr
		180						185					190		
Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn
		195					200					205			
His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys

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210	215	220
Arg Asp His Met Val Leu	Leu Glu Phe Val Thr	Ala Ala Gly Ile Thr
225	230	235 240
His Gly Met Asp Glu Leu Tyr Lys		
245		

<210> SEQ ID NO 27  
 <211> LENGTH: 248  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 27

Met Gly His His His His His Gly Gly Arg Ser Lys Gly Lys Arg		
1 5 10 15		
Leu Phe Arg Gly Lys Val Pro Ile Leu Val Lys Leu Lys Gly Asp Val		
20 25 30		
Asn Gly His Lys Phe Ser Val Arg Gly Lys Gly Lys Gly Asp Ala Thr		
35 40 45		
Arg Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro		
50 55 60		
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys		
65 70 75 80		
Phe Ser Arg Tyr Pro Lys His Met Lys Arg His Asp Phe Phe Lys Ser		
85 90 95		
Ala Met Pro Lys Gly Tyr Val Gln Glu Arg Thr Ile Ser Phe Lys Lys		
100 105 110		
Asp Gly Lys Tyr Lys Thr Arg Ala Glu Val Lys Phe Lys Gly Arg Thr		
115 120 125		
Leu Val Asn Arg Ile Lys Leu Lys Gly Arg Asp Phe Lys Glu Lys Gly		
130 135 140		
Asn Ile Leu Gly His Lys Leu Arg Tyr Asn Phe Asn Ser His Lys Val		
145 150 155 160		
Tyr Ile Thr Ala Asp Lys Arg Lys Asn Gly Ile Lys Ala Lys Phe Lys		
165 170 175		
Ile Arg His Asn Val Lys Asp Gly Ser Val Gln Leu Ala Lys His Tyr		
180 185 190		
Gln Gln Asn Thr Pro Ile Gly Arg Gly Pro Val Leu Leu Pro Arg Lys		
195 200 205		
His Tyr Leu Ser Thr Arg Ser Lys Leu Ser Lys Asp Pro Lys Glu Lys		
210 215 220		
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Lys		
225 230 235 240		
His Gly Arg Lys Glu Arg Tyr Lys		
245		

<210> SEQ ID NO 28  
 <211> LENGTH: 128  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 28

Ala Ala Glu Ala Gly Ile Thr Gly Thr Trp Tyr Asn Gln Leu Gly Ser
1 5 10 15

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Thr Phe Ile Val Thr Ala Gly Ala Asp Gly Ala Leu Thr Gly Thr Tyr  
                   20                  25                  30

Glu Ser Ala Val Gly Asn Ala Glu Ser Arg Tyr Val Leu Thr Gly Arg  
           35                  40                  45

Tyr Asp Ser Ala Pro Ala Thr Asp Gly Ser Gly Thr Ala Leu Gly Trp  
       50                  55                  60

Thr Val Ala Trp Lys Asn Asn Tyr Arg Asn Ala His Ser Ala Thr Thr  
   65                  70                  75                  80

Trp Ser Gly Gln Tyr Val Gly Gly Ala Glu Ala Arg Ile Asn Thr Gln  
           85                  90                  95

Trp Leu Leu Thr Ser Gly Thr Thr Glu Ala Asn Ala Trp Lys Ser Thr  
       100                  105                  110

Leu Val Gly His Asp Thr Phe Thr Lys Val Lys Pro Ser Ala Ala Ser  
       115                  120                  125

<210> SEQ ID NO 29  
 <211> LENGTH: 137  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 29

Met Gly His His His His His His Gly Gly Ala Glu Ala Gly Ile Thr  
 1                  5                  10                  15

Gly Thr Trp Tyr Asn Gln Leu Gly Ser Thr Phe Ile Val Thr Ala Gly  
           20                  25                  30

Ala Asp Gly Ala Leu Thr Gly Thr Tyr Glu Ser Ala Val Gly Asp Ala  
       35                  40                  45

Glu Ser Glu Tyr Val Leu Thr Gly Arg Tyr Asp Ser Ala Pro Ala Thr  
       50                  55                  60

Asp Gly Ser Gly Thr Ala Leu Gly Trp Thr Val Ala Trp Lys Asn Asp  
   65                  70                  75                  80

Tyr Glu Asn Ala His Ser Ala Thr Thr Trp Ser Gly Gln Tyr Val Gly  
           85                  90                  95

Gly Ala Glu Ala Arg Ile Asn Thr Gln Trp Leu Leu Thr Ser Gly Thr  
       100                  105                  110

Thr Glu Ala Asp Ala Trp Lys Ser Thr Leu Val Gly His Asp Thr Phe  
       115                  120                  125

Thr Lys Val Glu Pro Ser Ala Ala Ser  
       130                  135

<210> SEQ ID NO 30  
 <211> LENGTH: 137  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 30

Met Gly His His His His His His Gly Gly Ala Lys Ala Gly Ile Thr  
 1                  5                  10                  15

Gly Thr Trp Tyr Asn Gln Leu Gly Ser Thr Phe Ile Val Thr Ala Gly  
           20                  25                  30

Ala Lys Gly Ala Leu Thr Gly Thr Tyr Glu Ser Ala Val Gly Asn Ala  
       35                  40                  45

Lys Ser Arg Tyr Val Leu Thr Gly Arg Tyr Asp Ser Ala Pro Ala Thr  
       50                  55                  60

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Lys Gly Ser Gly Thr Ala Leu Gly Trp Thr Val Ala Trp Lys Asn Lys  
 65 70 75 80  
 Tyr Arg Asn Ala His Ser Ala Thr Thr Trp Ser Gly Gln Tyr Val Gly  
 85 90 95  
 Gly Ala Lys Ala Arg Ile Asn Thr Gln Trp Leu Leu Thr Ser Gly Thr  
 100 105 110  
 Thr Lys Ala Lys Ala Trp Lys Ser Thr Leu Val Gly His Asp Thr Phe  
 115 120 125  
 Thr Lys Val Lys Pro Ser Ala Ala Ser  
 130 135

<210> SEQ ID NO 31  
 <211> LENGTH: 442  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 31

ggttcagcca tgggtcatca ccaccacat cacggtggcg ccgaagcagg tattaccggt 60  
 acctgggtata accagttagg ctcaaccttt attgtgaccg cgggagcgga cggcgccctta 120  
 accggtacct acgaatcagc tgtaggtgac gcggaatcag agtacgtatt aaccggtcgt 180  
 tatgatagcg cgccggcgac tgacggtagc ggtactgctt taggttggac cgtagcgtgg 240  
 aagaatgatt atgaaaacgc acatagcgca acaacgtggt cagggcagta cgttggcgga 300  
 gctgaggcgc gcattaacac gcagtgggta ttaactagcg gcaccactga agctgatgcc 360  
 tggaagagca cgtttagtggg tcattgatacc ttcactaaag tggaaccttc agctgcgtca 420  
 taataatgac tcgagacctg ca 442

<210> SEQ ID NO 32  
 <211> LENGTH: 442  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 32

ggttcagcca tgggtcatca ccaccacat cacggtggcg ccaaagcagg tattaccggt 60  
 acctgggtata accagttagg ctcaaccttt attgtgaccg cgggagcgaa aggcgcctta 120  
 accggtacct acgaatcagc tgtaggaaac gcaaaatcac gctacgtatt aaccggtcgt 180  
 tatgatagcg cgccggcgac taaaggtagc ggtactgctt taggttggac cgtagcgtgg 240  
 aagaataagt atcgtaatgc gcacagtgc accacttggc cagggcagta cgtaggggga 300  
 gccaaagcac gtatcaacac gcagtgggta ttaacatcag gtaccaccaa agcgaaagcc 360  
 tggaagagca cgtttagtggg tcattgatacc ttcactaaag tgaaaccttc agctgcgtca 420  
 taataatgac tcgagacctg ca 442

<210> SEQ ID NO 33  
 <211> LENGTH: 217  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 33

Met Gly His His His His His His Gly Gly Pro Pro Tyr Thr Ile Thr



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1	5	10	15
Tyr Phe Pro Val Arg Gly Arg Cys Glu Ala Met Arg Met Leu Leu Ala	20	25	30
Asp Gln Asp Gln Ser Trp Lys Glu Glu Val Val Thr Met Glu Thr Trp	35	40	45
Pro Pro Leu Lys Pro Ser Cys Leu Phe Arg Gln Leu Pro Lys Phe Gln	50	55	60
Asp Gly Asp Leu Thr Leu Tyr Gln Ser Asn Ala Ile Leu Arg His Leu	65	70	80
Gly Arg Ser Phe Gly Leu Tyr Gly Lys Asp Gln Lys Glu Ala Ala Leu	85	90	95
Val Asp Met Val Asn Asp Gly Val Glu Asp Leu Arg Cys Lys Tyr Ala	100	105	110
Thr Leu Ile Tyr Thr Asn Tyr Glu Ala Gly Lys Glu Lys Tyr Val Lys	115	120	125
Glu Leu Pro Glu His Leu Lys Pro Phe Glu Thr Leu Leu Ser Gln Asn	130	135	140
Gln Gly Gly Gln Ala Phe Val Val Gly Ser Gln Ile Ser Phe Ala Asp	145	150	160
Tyr Asn Leu Leu Asp Leu Leu Arg Ile His Gln Val Leu Asn Pro Ser	165	170	175
Cys Leu Asp Ala Phe Pro Leu Leu Ser Ala Tyr Val Ala Arg Leu Ser	180	185	190
Ala Arg Pro Lys Ile Lys Ala Phe Leu Ala Ser Pro Glu His Val Asn	195	200	205
Arg Pro Ile Asn Gly Asn Gly Lys Gln	210	215	

&lt;210&gt; SEQ ID NO 34

&lt;211&gt; LENGTH: 217

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic Polypeptide

&lt;400&gt; SEQUENCE: 34

Met Gly His His His His His Gly Gly Pro Pro Tyr Thr Ile Thr	1	5	10	15
Tyr Phe Pro Val Arg Gly Arg Cys Glu Ala Met Arg Met Leu Leu Ala	20	25	30	
Asp Gln Asp Gln Ser Trp Glu Glu Glu Val Val Thr Met Glu Thr Trp	35	40	45	
Pro Pro Leu Lys Pro Ser Cys Leu Phe Arg Gln Leu Pro Lys Phe Gln	50	55	60	
Asp Gly Asp Leu Thr Leu Tyr Gln Ser Asn Ala Ile Leu Arg His Leu	65	70	75	80
Gly Arg Ser Phe Gly Leu Tyr Gly Glu Asp Glu Glu Glu Ala Ala Leu	85	90	95	
Val Asp Met Val Asn Asp Gly Val Glu Asp Leu Arg Cys Lys Tyr Ala	100	105	110	
Thr Leu Ile Tyr Thr Asp Tyr Glu Ala Gly Lys Glu Glu Tyr Val Glu	115	120	125	
Glu Leu Pro Glu His Leu Lys Pro Phe Glu Thr Leu Leu Ser Glu Asn	130	135	140	
Glu Gly Gly Glu Ala Phe Val Val Gly Ser Glu Ile Ser Phe Ala Asp				

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145	150	155	160
Tyr Asn Leu Leu Asp Leu Leu Arg Ile His Gln Val Leu Asn Pro Ser			
	165	170	175
Cys Leu Asp Ala Phe Pro Leu Leu Ser Ala Tyr Val Ala Arg Leu Ser			
	180	185	190
Ala Arg Pro Glu Ile Glu Ala Phe Leu Ala Ser Pro Glu His Val Asp			
	195	200	205
Arg Pro Ile Asn Gly Asn Gly Lys Gln			
	210	215	

<210> SEQ ID NO 35  
 <211> LENGTH: 217  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 35

Met Gly His His His His His His Gly Gly Pro Pro Tyr Thr Ile Thr			
1	5	10	15
Tyr Phe Pro Val Arg Gly Arg Cys Glu Ala Met Arg Met Leu Leu Ala			
	20	25	30
Asp Gln Lys Gln Ser Trp Lys Glu Glu Val Val Thr Met Lys Thr Trp			
	35	40	45
Pro Pro Leu Lys Pro Ser Cys Leu Phe Arg Gln Leu Pro Lys Phe Gln			
	50	55	60
Asp Gly Lys Leu Thr Leu Tyr Gln Ser Asn Ala Ile Leu Arg His Leu			
	65	70	75
Gly Arg Ser Phe Gly Leu Tyr Gly Lys Lys Gln Lys Glu Ala Ala Leu			
	85	90	95
Val Asp Met Val Asn Asp Gly Val Glu Asp Leu Arg Cys Lys Tyr Ala			
	100	105	110
Thr Leu Ile Tyr Thr Lys Tyr Lys Ala Gly Lys Lys Lys Tyr Val Lys			
	115	120	125
Lys Leu Pro Lys His Leu Lys Pro Phe Glu Thr Leu Leu Ser Lys Asn			
	130	135	140
Lys Gly Gly Lys Ala Phe Val Val Gly Ser Lys Ile Ser Phe Ala Asp			
	145	150	155
Tyr Asn Leu Leu Asp Leu Leu Arg Ile His Gln Val Leu Asn Pro Ser			
	165	170	175
Cys Leu Lys Ala Phe Pro Leu Leu Ser Ala Tyr Val Ala Arg Leu Ser			
	180	185	190
Ala Arg Pro Lys Ile Lys Ala Phe Leu Ala Ser Pro Glu His Val Lys			
	195	200	205
Arg Pro Ile Asn Gly Asn Gly Lys Gln			
	210	215	

<210> SEQ ID NO 36  
 <211> LENGTH: 682  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 36

ggttcagcca tgggtcatca ccaccaccat cacggtggcc cgccgtacac cattacatac	60
tttccggtac gtggtcggtg tgaagcgatg cgtatgttat tagcggacca ggaccaatca	120

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tgggaagaag aagtagtgac aatggaacc tggcgcgct taaagcctag ctgtttattc	180
cgtcaattac cgaagtttca ggatggtgat ttaaccttat accagtctaa cgcgatctta	240
cgtcatttag gtcgctcatt tggttttatac ggtgaagatg aagaagaagc agccttagtg	300
gatatggtga atgatggcgt ggaagactta cgttgtaaat acgcgacgtt aatttacact	360
gattatgaag ccggtaaaga ggagtacgtg gaagaattac ctgaacacct gaagccgttt	420
gaaacattac tgagcgaaaa tgaaggaggt gaggcgttcg tagttggtag cgaaattagc	480
ttcgctgatt ataacttatt agacttatta cgcattcacc aggtttttaa tcctagctgt	540
ttagacgctt tcccgttact gagcgcatat gtagcgcgcc tgagcgcccg tccggaatt	600
gaagctttct tagcgtcacc tgaacacgtg gaccgcccga ttaacggaaa cggcaagcag	660
taataatgag gtaccacctg ca	682

<210> SEQ ID NO 37  
 <211> LENGTH: 682  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 37

ggttcagcca tgggtcatca ccaccacat caggtggcc cgccgtacac cattacatac	60
tttccggtac gtggtcgttg tgaagcgatg cgtatgttat tagcggacca gaaacaatca	120
tgggaagaag aagtagtgac aatgaagacc tggcgcgct taaagcctag ctgtttattc	180
cgtcaattac cgaagtttca ggatggtaaa ttaaccttat accagtctaa cgcgatctta	240
cgtcatttag gtcgctcatt tggttttatac ggtaagaagc agaaagaagc agccttagtg	300
gatatggtga atgatggcgt ggaagactta cgttgtaaat acgcgacgtt aatttacact	360
aaatataaag ccggtaaaaa gaagtacgtg aaaaaattac ctaaacacct gaagccgttt	420
gaaacattac tgagcaaaaa taaaggaggt aaggcgttcg tagttggtag caagattagc	480
ttcgctgatt ataacttatt agacttatta cgcattcacc aggtttttaa tcctagctgt	540
ttaaaggctt tcccgttact gagcgcatat gtagcgcgcc tgagcgcccg tccgaagatc	600
aaagctttct tagcgtcacc tgaacacgtg aagcgcccga ttaacggaaa cggcaagcag	660
taataatgag gtaccacctg ca	682

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What is claimed is:

1. A supercharged protein variant of a wild-type protein, wherein the supercharged protein variant comprises a modified primary amino acid sequence as compared to the wild-type sequence, resulting in a theoretical net charge on the supercharged protein variant of +10 to +52 at physiological pH, wherein the theoretical net charge at physiological pH of the supercharged protein variant is increased by at least +3 as compared to the theoretical net charge of the wild-type protein,

wherein the wild-type protein is an immunoglobulin or a fragment thereof.

2. The supercharged protein of claim 1, wherein the theoretical net charge at physiological pH of the supercharged protein variant is increased by at least +4, at least +5, at least +10, at least +15, at least +20, at least +25, at least +30, or at least +35 as compared to the theoretical net charge of the wild-type sequence.

3. The supercharged protein variant of claim 1, wherein the theoretical net charge at physiological pH of the supercharged protein is within the range of +52 to +20, +52 to +30, or +52 to +40.

4. The supercharged protein variant of claim 1, wherein the supercharged protein variant retains at least 50%, at least 75%, at least 90%, or at least 95% of the activity of the wild-type protein.

5. The supercharged protein variant of claim 1, wherein the wild-type protein is an immunoglobulin.

6. The supercharged protein variant of claim 1, wherein the immunoglobulin or fragment thereof is human or humanized.

7. The supercharged protein variant of claim 1, wherein the variant is a fusion protein.

8. The supercharged protein variant of claim 7, wherein the fusion protein comprises a linker.

9. The supercharged protein variant of claim 1, wherein the modified primary amino acid sequence of the super-

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charged protein variant comprises a replacement of at least one charged surface residue of the wild-type protein with a different residue.

10. The supercharged protein variant of claim 1, wherein the modified primary amino acid sequence of the supercharged protein variant comprises a replacement of at least one surface residue of the wild-type protein with a lysine, histidine, or arginine residue.

11. The supercharged protein variant of claim 1, wherein the modified primary amino acid sequence of the supercharged protein variant comprises a replacement of at least two, at least five, at least ten, at least twenty, or at least thirty surface residues of the wild-type protein with a different residue.

12. A composition comprising the supercharged protein variant of claim 1.

13. The supercharged protein variant of claim 1, wherein the wild-type protein is a fragment of an immunoglobulin.

14. The supercharged protein variant of claim 1, wherein the modified primary amino acid sequence comprises replacing a plurality of non-conserved, surface residues with a natural amino acid residue that is positively charged at physiological pH; and wherein non-conserved, surface residues are identified by comparing the amino acid sequence of the protein with at least one other amino acid sequence of the protein from the same protein family or a different species, wherein a residue is non-conserved if less than or equal to 50% of the amino acid sequences have the same amino acid sequence in a particular position.

15. A method of preparing a supercharged protein variant of claim 1, the method comprising steps of:

identifying the surface residues of a protein of interest that are not highly conserved among other proteins related to the protein of interest; and

replacing a plurality of non-conserved, surface residues with an amino acid residue that is positively charged at physiological pH, or

replacing a plurality of non-conserved, surface residues with an amino acid residue that is negatively charged at physiological pH.

16. A supercharged protein variant of a wild-type protein, wherein the supercharged protein variant comprises a modified primary amino acid sequence as compared to the wild-type sequence, resulting in a theoretical net charge on the supercharged protein variant of -40 to -10 at physiological pH, wherein the theoretical net charge at physiological pH of the supercharged protein variant is decreased by at least -3 as compared to the theoretical net charge of the wild-type protein,

wherein the wild-type protein is an immunoglobulin or a fragment thereof.

17. The supercharged protein of claim 16, wherein the theoretical net charge at physiological pH of the supercharged protein variant is decreased by at least -4, at least -5, at least -10, at least -15, at least -20, at least -25, at least -30, or at least -35 as compared to the theoretical net charge of the wild-type sequence.

18. The supercharged protein variant of claim 16, wherein the theoretical net charge at physiological pH of the supercharged protein is within the range of -40 to -20 or -40 to -30.

19. The supercharged protein variant of claim 16, wherein the modified primary amino acid sequence of the supercharged protein variant comprises a replacement of at least one charged surface residue of the wild-type protein with a different residue.

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20. The supercharged protein variant of claim 16, wherein the modified primary amino acid sequence of the supercharged protein variant comprises a replacement of at least one surface residue of the wild-type protein with an aspartate or glutamate residue.

21. The supercharged protein variant of claim 16, wherein the wild-type protein is an immunoglobulin.

22. The supercharged protein variant of claim 16, wherein the wild-type protein is a fragment of an immunoglobulin.

23. The supercharged protein variant of claim 16, wherein the immunoglobulin or fragment thereof is human or humanized.

24. The supercharged protein variant of claim 16, wherein the modified primary amino acid sequence comprises replacing a plurality of non-conserved, surface residues with a natural amino acid residue that is positively charged at physiological pH; and wherein non-conserved, surface residues are identified by comparing the amino acid sequence of the protein with at least one other amino acid sequence of the protein from the same protein family or a different species, wherein a residue is non-conserved if less than or equal to 50% of the amino acid sequences have the same amino acid sequence in a particular position.

25. A protein selected from:

a green fluorescent protein (+36 GFP) comprising the amino acid sequence: MGHHHHHHGGASKGERLFRGKVPILVELKGDVNGHKFSVRGKGKGDATRGKLTLLKFICTT GKLPVPWPTLVTTLTLYGVQCF-SRYPKHKMRHDFFKSAMPKGYVQERTISFKKDGKYKTRA EVKFEGRTLNVNRIKLKGRDFKEKG-NILGHKLRYNFNSHKVYITADKRKNIGIAKFKIRHNV KDGSVQLADHYQQNTPIGRGPVLLPRNHYLSTRSKLSKDPKEKRDHMLLEFVTAAGIKHGRDERYK (SEQ ID NO: 5);

a green fluorescent protein (+42 GFP) comprising the amino acid sequence: MGHHHHHHGGRSKGGKRLFRGKVPILVELKGDVNGHKFSVRGKGKGDATRGKLTLLKFICT TGKLPVPWPTLVTTLTLYGVQCF-SRYPKHKMRHDFFKSAMPKGYVQERTISFKKDGKYKTR AEVKFEGRTLNVNRIKLKGRDFKEKG-NILGHKLRYNFNSHKVYITADKRKNIGIAKFKIRHN VKDGSVQLADHYQQNTPIGRGPVLLPRKHYLSTRSKLSKDPKEKRDHMLLEFVTAAGIKHGRKERYK (SEQ ID NO: 6);

a green fluorescent protein (+48 GFP) comprising the amino acid sequence: MGHHHHHHGGRSKGGKRLFRGKVPILVKLKGDVNGHKFSVRGKGKGDATRGKLTLLKFICT TGKLPVPWPTLVTTLTLYGVQCF-SRYPKHKMRHDFFKSAMPKGYVQERTISFKKDGKYKTR AEVKFKGRTLNVNRIKLKGRDFKEKG-NILGHKLRYNFNSHKVYITADKRKNIGIAKFKIRHN VKDGSVQLAKHYQQNTPIGRGPVLLPRKHYLSTRSKLSKDPKEKRDHMLLEFVTAAGIKHGRKERYK (SEQ ID NO: 27);

a green fluorescent protein (+49 GFP) comprising the amino acid sequence: MGHHHHHHGGRSKGGKRLFRGKVPILVKLKGDVNGHKFSVRGKGKGDATRGKLTLLKFICT TGKLPVPWPTLVTTLTLYGVQCF-SRYPKHKMRHDFFKSAMPKGYVQERTISFKKDGKYKTR AEVKFKGRTLNVNRIKLKGRDFKEKG-NILGHKLRYNFNSHKVYITADKRKNIGIAKFKIRHN VKDGSVQLAKHYQQNTPIGRGPVLLPRKHYLSTRSKLSKDPKEKRDHMLLEFVTAAGIKHGRKERYK (SEQ ID NO: 7);

a streptavidin (+52 SAV) comprising an amino acid sequence: MGHHHHHHGGAKAGITGTWYNQLG-

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- STFIVTAGAKGALTGTYESAVGNAKSRYVLT-GRYD SAPATKSGTALGWTVAWKNKYRNAH-SATTWSGQYVGGAKARINTQWLLTSGTTKAKA WKSTLVGHDTFTKVKPSAAS (SEQ ID NO: 30); and
- a glutathione-S-transferase (+50 GST) of amino acid sequence: MGHHHHHHGGPPYTITTYFPVRGRCEA-MRMLLADQKQSWKEEVVTMKTWPPLKPSCL-FRQ LPKFQDGLTLYQSNAILRHLGRSFGLYGK-KQKEAALVDMVNDGVEDLRCKYATLIYTKY KAGKKKYVKLPKHLKPFETLLSKNKGKGAFFV-VGSKISFADYNLLDLLRIHQVLNPSCLKA FPLL-SAYVARLSARPKIAFLASPEHVKRPINGNGKQ (SEQ ID NO: 35).
26. A supercharged protein selected from:
- a streptavidin protein (−40 SAV) comprising an amino acid sequence: MGHHHHHHGGAEAGITGTWYN-QLGSTFIVTAGADGALTGTYESAVGDAESEYV-LTGRYD SAPATDGSALTALGWTVAWKNDYENAH-SATTWSGQYVGGAEARINTQWLLTSGTTEA-DA WKSTLVGHDTFTKVEPSAAS (SEQ ID NO: 29);
- a green fluorescent protein (−30 GFP) of amino acid sequence: MGHHHHHHGGASKGEELFDGVVPIL-VELDGDVNGHEFSVRGEGEGDATEGELTLK-FICTT GELPVPWPPTLVTTLTLYGVQCFSRYPDHM-DQHDFFKSAMPEGYVQERTISFKDDGTYKTRA EVKFEGDTLVNRIELKGIDFKEDGNILGHK-LEYNFNSHDVYITADKQENGKAFFEIRHNVE DGSVQLADHYQQNTPIGDGPVLLPDDHYLSTE-SALSKDPNEDRDHMLLEFVTAAGIDHG MDE-LYK (SEQ ID NO: 4);

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- a green fluorescent protein (−29 GFP) of amino acid sequence: MGHHHHHHGGASKGEELFDGEVPIL-VELDGDVNGHEFSVRGEGEGDATEGELTLK-FICTT GELPVPWPPTLVTTLTLYGVQCFSRYPDHM-DQHDFFKSAMPEGYVQERTISFKDDGTYKTRA EVKFEGDTLVNRIELKGIDFKEDGNILGHK-LEYNFNSHDVYITADKQENGKAFFEIRHNVE DGSVQLADHYQQNTPIGDGPVLLPDDHYLSTE-SALSKDPNEDRDHMLLEFVTAAGIDHG MDE-LYK (SEQ ID NO: 3);
- a green fluorescent protein (−25 GFP) of amino acid sequence: MGHHHHHHGGASKGEELFTGVVPIL-VELDGDVNGHEFSVRGEGEGDATEGELTLK-FICTT GELPVPWPPTLVTTLTLYGVQCFSRYPDHM-KQHDFFKSAMPEGYVQERTISFKDDGTYKTRA EVKFEGDTLVNRIELKGIDFKEDGNILGHK-LEYNFNSHDVYITADKQENGKAFFEIRHNVE DGSVQLADHYQQNTPIGDGPVLLPDDHYLSTE-SALSKDPNEDRDHMLLEFVTAAGIDHG MDE-LYK (SEQ ID NO: 2); and
- a glutathione-S-transferase (−40 GST) of amino acid sequence: MGHHHHHHGGPPYTITTYFPVRGRCEA-MRMLLADQDQSWEEVVVTMETWPPLKPSCL-FRQ LPKFQDGLTLYQSNAILRHLGRSFGLY-GEDEEEAALVDMVNDGVEDLRCKYATLIYTDY EAGKEEYVEELPEHLKPFETLLSENEGGEAFV-VGSEISFADYNLLDLLRIHQVLNPSCLDAFP LLSAYVARLSARPEIEAFLASPEHVDRP-INGNGKQ (SEQ ID NO: 34).

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